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(54) Title: HUMAN PROSTATE CANCER ASSOCIATED GENE SEQUENCES AND POLYPEPTIDES

(57) Abstract

This invention relates to newly identified prostate or prostate cancer related polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "prostate cancer antigens", and to the complete gene sequences associated therewith and to the expression products thereof, as well as the use of such prostate cancer antigens for detection, prevention and treatment of disorders of the prostate, particularly the presence of prostate cancer. This invention relates to the prostate cancer antigens as well as vectors, host cells, antibodies directed to prostate cancer antigens and recombinant and synthetic methods for producing the same. Also provided are diagnostic methods for diagnosing and treating, preventing and/or prognosing disorders related to the prostate, including prostate cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of prostate cancer antigens of the invention. The present invention further relates to methods and/or compositions for inhibiting the production and/or function of the polypeptides of the present invention.

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Human Prostate Cancer Associated Gene Sequences and Polypeptides

Field of the Invention

This invention relates to newly identified prostate or prostate cancer related polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "prostate cancer antigens," and to the complete gene sequences associated therewith and to the expression products thereof, as well as the use of such prostate cancer antigens for detection, prevention and treatment of disorders of the prostate, particularly the presense of prostate cancer. This invention relates to the prostate cancer antigens as well as vectors, host cells, antibodies directed to prostate cancer antigens and recombinant and synthetic methods for producing the same. Also provided are diagnostic methods for diagnosing and treating, preventing and/or prognosing disorders related to the prostate, including prostate cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of prostate cancer antigens of the invention. The present invention further relates to methods and/or compositions for inhibiting the production and/or function of the polypeptides of the present invention.

Background of the Invention

Cell growth is a carefully regulated process which responds to specific needs of the body. Occassionally, the intricate, and highly regulated controls dictating the rules for cellular division break down. When this occurs, the cell begins to grow and divide independently of its homeostatic regulation resulting in a condition commonly referred to as cancer. In fact, cancer is the second leading cause of death among Americans aged 25-44.

Prostate cancer has become the most common cancer among American men, and only lung cancer is responsible for more cancer deaths (Boring, Cancer Statistics, 41:19-36 (1991)). The age specific mortality rate has slowly increased over the past 50 years and in black American men is nearly double the rate found in white men (Carter, Prostate,

16:39-48 (1990)). Prostate cancer is responsible for nearly three percent of all deaths in men over the age of 55 years (Seidman, et al., Probabilities of Eventually Developing or Dying of Cancer-United States, 35:36-56 (1985)). Since the incidence of prostate cancer increases more rapidly with age than any other cancer, and the average age of American men is rising, the number of patients with prostate cancer is expected to increase dramatically over the next decade.

Approximately 30% of men with prostate cancer have distant metastases at the time of diagnosis (Schmidt, et al., J. Urol., 136:416-421 (1986)). Despite the impressive symptomatic response of metastases to hormonal manipulation (androgen deprivation), the survival rate for these patients is dismal: the median duration of survival is less than three years (Eyar, Urologic Pathology: The Prostate, Philadelphia, Pa., Lea and Febiger, 241-267 (1977)). By five years, over 75% and by ten years, more than 90% of these patients die of their cancer rather than with it (Silverberg, Cancer, 60:692-717 (1987) (Suppl.)). The problem with prostate cancer is that many forms of prostate cancer are latent, in other words, such forms are difficult to detect. Approximately 30% of the men over the age of 50 years who have no clinical evidence of prostate cancer harbor foci of cancer within the prostate (McNeal, et al., The Lancet, January, 11:60-63 (1986)). This remarkably high prevalence of prostate cancer at autopsy, seen in no other organ, makes it the most common malignancy in human beings (Dhom, J. Cancer Res. Clin. Oncol., 106:210-218 (1983)). There is strong support for the concept of multi-step process in the pathogenesis of prostate cancer in which latent cancers progress through some but not all of the steps necessary for full malignant expression (Utter, et al., J. Urol., 143:742-746 (1990).

There are a variety of techniques for early detection and characteristics of prostate cancers, however, none of them are devoid of problems. Prostate cancer is a notoriously silent disease with few early symptoms. There is a need, therefore, for identification and characterization of factors that modulate activation and differentiation of prostate cells, both normally and in disease states. In particular, there is a need to isolate and characterize additional molecules that mediate apoptosis, DNA repair, tumor-mediated angiogenesis, genetic imprinting, immune responses to tumors and tumor antigens and, among other things, that can play a role in detecting, preventing, ameliorating or correcting dysfunctions or diseases related to the prostate.

Summary of the Invention

The present invention includes isolated nucleic acid molecules comprising, or alternatively, consisting of, a prostate and/or prostate cancer associated polynucleotide sequence disclosed in the sequence listing (as SEQ ID Nos:1 to 940) and/or contained in a human cDNA clone described in Tables 1, 2 and 5 and deposited with the American Type Culture Collection ("ATCC"). Fragments, variant, and derivatives of these nucleic acid molecules are also encompassed by the invention. The present invention also includes isolated nucleic acid molecules comprising, or alternatively consisting of, a polynucleotide encoding a prostate or prostate cancer polypeptide. The present invention further includes prostate and/or prostate cancer polypeptides encoded by these polynucleotides. Further provided for are amino acid sequences comprising, or alternatively consisting of, prostate and/or prostate cancer polypeptides as disclosed in the sequence listing (as SEQ ID Nos: 941 to 1880) and/or encoded by a human cDNA clone described in Tables 1, 2 and 5 and deposited with the ATCC. Antibodies that bind these polypeptides are also encompassed by the invention. Polypeptide fragments, variants, and derivatives of these amino acid sequences are also encompassed by the invention, as are polynucleotides encoding these polypeptides and antibodies that bind these polypeptides. Also provided are diagnostic methods for diagnosing and treating, preventing, and/or prognosing disorders related to the prostate, including prostate cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of prostate cancer antigens of the invention.

Detailed Description

Tables

Table 1 summarizes some of the prostate cancer antigens encompassed by the invention (including contig sequences (SEQ ID NO:X) and the cDNA clone related to the contig sequence) and further summarizes certain characteristics of the prostate cancer polynucleotides and the polypeptides encoded thereby. The first column shows the "SEQ ID NO:" for each of the 940 prostate cancer antigen polynucleotide sequences of the invention. The second column provides a unique "Sequence/Contig ID" identification for

each prostate and/or prostate cancer associated sequence. The third column, "Gene Name," and the fourth column, "Overlap," provide a putative identification of the gene based on the sequence similarity of its translation product to an amino acid sequence found in a publicly accessible gene database and the database accession no. for the database sequence having similarity, respectively. The fifth and sixth columns provide the location (nucleotide position nos. within the contig), "Start" and "End", in the polynucleotide sequence "SEQ ID NO:X" that delineate the preferred ORF shown in the sequence listing as SEQ ID NO:Y. The seventh and eighth columns provide the "% Identity" (percent identity) and "% Similarity" (percent similarity), respectively, observed between the aligned sequence segments of the translation product of SEQ ID NO:X and the database sequence. The ninth column provides a unique "Clone ID" for a cDNA clone related to each contig sequence.

Table 2 summarizes ATCC Deposits, Deposit dates, and ATCC designation numbers of deposits made with the ATCC in connection with the present application.

Table 3 indicates public ESTs, of which at least one, two, three, four, five, ten, fifteen or more of any one or more of these public EST sequences are optionally excluded from certain embodiments of the invention.

Table 4 lists residues comprising antigenic epitopes of antigenic epitope-bearing fragments present in most of the prostate or prostate cancer associated polynucleotides described in Table 1 as predicted by the inventors using the algorithm of Jameson and Wolf, (1988) Comp. Appl. Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power MacIntosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). Prostate and prostate cancer associated polypeptides (e.g., SEQ ID NO:Y, polypeptides encoded by SEQ ID NO:X, or polypeptides encoded by the cDNA in the referenced cDNA clone) may possess one or more antigenic epitopes comprising residues described in Table 4. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly. The residues and locations shown in column two of Table 4 correspond to the amino acid sequences for most prostate and prostate cancer associated polypeptide sequence shown in the Sequence Listing.

Table 5 shows the cDNA libraries sequenced, and ATCC designation numbers

and vector information relating to these cDNA libraries.

Definitions

The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide. The term "isolated" does not refer to genomic or cDNA libraries, whole cell total or mRNA preparations, genomic DNA preparations (including those separated by electrophoresis and transferred onto blots), sheared whole cell genomic DNA preparations or other compositions where the art demonstrates no distinguishing features of the polynucleotide/sequences of the present invention.

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:X (as described in column 1 of Table 1) or the related cDNA clone (as described in column 9 of Table 1 and contained within a library deposited with the ATCC). For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having an amino acid sequence encoded by a polynucleotide of the invention as broadly defined (obviously excluding poly-Phenylalanine or poly-Lysine peptide sequences which result from translation of a polyA tail of a sequence corresponding to a cDNA).

In the present invention, "SEQ ID NO:X" was often generated by overlapping sequences contained in multiple clones (contig analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X is deposited at Human Genome Sciences, Inc. (HGS) in a catalogued and archived library. As shown in column 9 of Table 1, each clone is identified by a cDNA Clone ID. Each Clone ID is unique to an

individual clone and the Clone ID is all the information needed to retrieve a given clone from the HGS library. In addition to the individual cDNA clone deposits, most of the cDNA libraries from which the clones were derived were deposited at the American Type Culture Collection (hereinafter "ATCC"). Table 5 provides a list of the deposited cDNA libraries. One can use the Clone ID to determine the library source by reference to Tables 2 and 5. Table 5 lists the deposited cDNA libraries by name and links each library to an ATCC Deposit. Library names contain four characters, for example, "HTWE." The name of a cDNA clone ("Clone ID") isolated from that library begins with the same four characters, for example "HTWEP07". As mentioned below, Table 1 correlates the Clone ID names with SEQ ID NOs. Thus, starting with a SEQ ID NO, one can use Tables 1, 2 and 5 to determine the corresponding Clone ID, from which library it came and in which ATCC deposit the library is contained. Furthermore, it is possible to retrieve a given cDNA clone from the source library by techniques known in the art and described elsewhere herein. The ATCC is located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. The ATCC deposits were made persuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for the purposes of patent procedure.

A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:X, or the complement thereof (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments described herein), and/or sequences contained in the related cDNA clone within a library deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42 degree C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65 degree C.

Also included within "polynucleotides" of the present invention are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt

conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37 degree C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH_2PO_4; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 ug/ml salmon sperm blocking DNA; followed by washes at 50 degree C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

Of course, a polynucleotide which hybridizes only to polyA+ sequences (such as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone generated using oligo dT as a primer).

The polynucleotides of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

In specific embodiments, the polynucleotides of the invention are at least 15, at least 30, at least 50, at least 100, at least 125, at least 500, or at least 1000 continuous nucleotides but are less than or equal to 300 kb, 200 kb, 100 kb, 50 kb, 15 kb, 10 kb, 7.5kb, 5 kb, 2.5 kb, 2.0 kb, or 1 kb, in length. In a further embodiment, polynucleotides of the invention comprise a portion of the coding sequences, as disclosed herein, but do not comprise all or a portion of any intron. In another embodiment, the polynucleotides comprising coding sequences do not contain coding sequences of a genomic flanking gene (i.e., 5' or 3' to the gene of interest in the genome). In other embodiments, the polynucleotides of the invention do not contain the coding sequence of more than 1000, 500, 250, 100, 50, 25, 20, 15, 10, 5, 4, 3, 2, or 1 genomic flanking gene(s).

"SEQ ID NO:X" refers to a prostate cancer antigen polynucleotide sequence described in Table 1. SEQ ID NO:X is identified by an integer specified in column 1 of Table 1. The polypeptide sequence SEQ ID NO:Y is a translated open reading frame (ORF) encoded by polynucleotide SEQ ID NO:X. There are 940 prostate cancer antigen polynucleotide sequences described in Table 1 and shown in the sequence listing (SEQ ID NO:1 through SEQ ID NO:940). Likewise there are 940 polypeptide sequences shown in the sequence listing, one polypeptide sequence for each of the polynucleotide sequences (SEQ ID NO:941 through SEQ ID NO:1880). The polynucleotide sequences are shown in the sequence listing immediately followed by all of the polypeptide sequences. Thus, a polypeptide sequence corresponding to polynucleotide sequence SEQ ID NO:1 is the first polypeptide sequence shown in the sequence listing. The second polypeptide sequence corresponds to the polynucleotide sequence shown as SEQ ID NO:2, and so on. In otherwords, since there are 940 polynucleotide sequences, for any polynucleotide sequence SEQ ID NO:X, a corresponding polypeptide SEQ ID NO:Y can be determined by the formula X + 940 = Y. In addition, any of the unique "Sequence/Contig ID" defined in column 2 of Table 1, can be linked to the corresponding polypeptide SEQ ID NO:Y by reference to Table 4.

The polypeptides of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications

are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth Enzymol 182:626-646 (1990); Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

The prostate and prostate cancer polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below). It is often advantageous to include an additional amino acid sequence which contains secretory or

leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

The prostate and prostate cancer polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified using techniques described herein or otherwise known in the art, such as, for example, by the one-step method described in Smith and Johnson, Gene 67:31-40 (1988). Polypeptides of the invention also can be purified from natural, synthetic or recombinant sources using techniques described herein or otherwise known in the art, such as, for example, antibodies of the invention raised against the polypeptides of the present invention in methods which are well known in the art.

By a polypeptide demonstrating a "functional activity" is meant, a polypeptide capable of displaying one or more known functional activities associated with a full-length (complete) protein of the invention. Such functional activities include, but are not limited to, biological activity, antigenicity [ability to bind (or compete with a polypeptide for binding) to an anti-polypeptide antibody], immunogenicity (ability to generate antibody which binds to a specific polypeptide of the invention), ability to form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide.

"A polypeptide having functional activity" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular assay, such as, for example, a biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention).

The functional activity of the prostate cancer antigen polypeptides, and fragments, variants derivatives, and analogs thereof, can be assayed by various methods.

For example, in one embodiment where one is assaying for the ability to bind or compete with full-length polypeptide of the present invention for binding to an antibody to the full length polypeptide antibody, various immunoassays known in the art can be used, including but not limited to, competitive and non-competitive assay systems using techniques such as radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitation reactions, immunodiffusion assays, in situ immunoassays (using colloidal gold, enzyme or radioisotope labels, for example), western blots, precipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc. In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labeled. Many means are known in the art for detecting binding in an immunoassay and are within the scope of the present invention.

In another embodiment, where a ligand is identified, or the ability of a polypeptide fragment, variant or derivative of the invention to multimerize is being evaluated, binding can be assayed, e.g., by means well-known in the art, such as, for example, reducing and non-reducing gel chromatography, protein affinity chromatography, and affinity blotting. See generally, Phizicky, E., et al., Microbiol. Rev. 59:94-123 (1995). In another embodiment, physiological correlates polypeptide of the present invention binding to its substrates (signal transduction) can be assayed.

In addition, assays described herein (see Examples) and otherwise known in the art may routinely be applied to measure the ability of polypeptides of the present invention and fragments, variants derivatives and analogs thereof to elicit polypeptide related biological activity (either in vitro or in vivo). Other methods will be known to the skilled artisan and are within the scope of the invention.

Prostate and Prostate Cancer Associated Polynucleotides and Polypeptides of the Invention

It has been discovered herein that the polynucleotides described in Table 1 are expressed at significantly enhanced levels in human prostate and/or prostate cancer tissues. Accordingly, such polynucleotides, polypeptides encoded by such polynucleotides, and antibodies specific for such polypeptides find use in the prediction, diagnosis, prevention and treatment of prostate related disorders, including prostate cancer as more fully described below.

Table 1 summarizes some of the polynucleotides encompassed by the invention (including contig sequences (SEQ ID NO:X) and the related cDNA clones) and further summarizes certain characteristics of these prostate and/or prostate cancer associated polynucleotides and the polypeptides encoded thereby.

Table 1

Seq ID No.	Sequence/ Contig ID	Gene Name	Overlap	HGS Nucleotide Start	HGS Nucleotide End	% Identity	% Similarity	Clone ID
1	574130	(AJ223500) nidogen-2 [Homo sapiens] Length = 1375	gnl|PID|e1237850	3	716	87	87	HOEOC56
2	637706			3	1025			HJAAT54
3	638162			109	696			HNTMW23
4	684310			10	300			HFXJA96
5	731016	protease [Human endogenous retrovirus K] >sp|P87892|P87892 PROTEASE (FRAGMENT). Length = 334	gnl|PID|e290663	2	370	66	83	HPLBP54
6	827771			188	322			HPFCR50
7	828193	MAGE-3b [Homo sapiens] >gi|533523 MAGE-6 antigen [Homo sapiens] >gnl|PID|d1007417 MAGE-6 protein [Homo sapiens]	gi|499122	237	716	97	97	HMMBI07
8	828194			243	401			HPKAA18
9	828199			2	463			HPJCU04
10	828221	put. LAR preprotein (AA -16 to 1881) [Homo sapiens] >pir|S03841|TDHULK leukocyte antigen-related protein precursor - human Length = 1897	gi|34267	1	1326	100	100	HWHQP39
11	828235			3	248			HWBBB77
12	828236	Gu protein [Homo sapiens] >pir|PC6010|PC6010 RNA helicase Gu - human (fragment) >sp|Q13436|Q13436 NUCLEOLAR RNA HELICASE GU (FRAGMENT). Length = 801	gi|1230564	1	1425	84	84	HWBDP29
13	828237			3	779			HWHPW78

14	828239	(AC002451) pyruvate dehydrogenase kinase isoform 4 [Homo sapiens] >gi|1399197 pyruvate dehydrogenase kinase isoform 4 [Homo sapiens]	gi|2337883	2	433	87	87	HWACS81
15	828242	(AF044321) cytochrome c oxidase assembly protein COX11 [Homo sapiens] >gi|3170264 (AF044321) cytochrome c oxidase assembly protein COX11 [Homo sapiens]	gi|3170264	3	731	100	100	HWBAS37
16	828247	(AF109906) NG22 [Mus musculus] Length = 707	gi|3986770	3	554	39	61	HWBBX45
17	828248	M1 subunit of ribonucleotide reductase [Homo sapiens] >gi|36153 large subunit ribonucleotide reductase [Homo sapiens] >pir|S16680|S16680 ribonucleoside-diphosphate reductase (EC 1.17.4.1) chain M1 - human Length = 792	gi|36065	254	625	82	82	HWBAJ23
18	828250			58	408			HWBBN56
19	828256	put. ribosomal protein L3 (AA 1 - 348) [Homo sapiens] >pir|A27294|R5HUL3 ribosomal protein L3 precursor, mitochondrial - human Length = 348	gi|34754	393	1193	94	94	HUSGZ25
20	828267			3	497			HUSIK57
21	828269			214	492			HUSBF75
22	828272			89	607			HUSYB27
23	828273	(AF047020) alpha-methylacyl-CoA racemase [Homo sapiens] >sp|O43673|O43673 ALPHA-METHYLACYL-COA RACEMASE (EC 5.1.99.4). Length = 380	gi|2896148	300	539	79	89	HULCJ25
24	828290			648	914			HUSGH59
25	828326	Ki antigen [Mus musculus] >gnl|PID|d1029778 (AB007139) PA28 gamma subunit [Mus musculus] >sp|O35563|O35563 KI ANTIGEN. Length = 254	gnl|PID|d1022900	2	970	99	99	HTXJJ72

26	828397			1	942			HLYCG48
27	828405	smooth muscle myosin light chain kinase, smMLCK {C-terminal} [sheep, myometrial tissue, day 127 of gestation, Peptide Partial, 438 aa] [Ovis aries] Length = 438	bbs|175341	37	579	98	100	HLDBK03
28	828461	fra-1 gene product (AA 1-271) [Homo sapiens] >pir|S15750|S15750 transforming protein (fra-1) - human >sp|P15407|FRA1_HUMAN FOS-RELATED ANTIGEN 1. Length = 271	gi|31463	1	873	71	71	HSKEI92
29	828482	Gephyrin [Rattus norvegicus] >pir|JH0681|JH0681 gephyrin - rat >sp|Q03555|GEPH_RAT GEPHYRIN (PUTATIVE GLYCINE RECEPTOR-TUBULIN LINKER PROTEIN). Length = 736	gi|56312	2	940	98	98	HSIGE72
30	828488			64	189			HSDJR78
31	828491			386	586			HSDFC18
32	828492			51	212			HSDGQ64
33	828494			428	733			HSDIC05
34	828496	BS4 peptide [Mus musculus] >sp|P54729|BS4_MOUSE BS4 PROTEIN. Length = 677	gi|863014	3	1097	85	93	HSBAY13
35	828498	14.5 kDa translational inhibitor protein, p14.5 [Homo sapiens] Length = 137	gnl|PID|e1240168	63	500	100	100	HSDXA60
36	828504			173	412			HSAAQ28
37	828507			286	462			HSBCA90
38	828512	CCAAT-box-binding factor [Homo sapiens] >pir|A36368|A36368 transcription factor CBF, CCAAT-binding - human	gi|179969	3	611	82	82	HSAAV04
39	828516	histone H2A [Homo sapiens] >gi|206270|histone 2A-like protein [Homo sapiens] >gi|2088554 histone 2A-like protein [Homo sapiens]	gnl|PID|e268230	36	458	100	100	HSBAL82

40	828519			142	474			HRGBO34
41	828521	DEAD box-like RNA helicase [Arabidopsis thaliana] >sp|O23251|O23251 DEAD BOX-LIKE RNA HELICASE (FRAGMENT). Length = 450	gnl|PID|e1316345	31	531	38	58	HRGDE67
42	828522	Unknown		361	684			HROBP89
43	828525	cytokine receptor [Homo sapiens] >sp|Q14213|Q14213 CYTOKINE RECEPTOR PRECURSOR.	gi|632974	14	463	99	99	HRGTJ13
44	828529			379	852			HROEB35
45	828530			134	253			HRACZ50
46	828536			84	272			HPYSC02
47	828537			1	270			HPZAA72
48	828539			130	279			HPWDG48
49	828540	ORF_f506 [Escherichia coli] >gi|1789453 (AE000389) aerotaxis sensor receptor, flavoprotein [Escherichia coli]	gi|882594	3	278	100	100	HPWCG66
50	828542			366	626			HRAAA23
51	828543	(AF093263) homer-2a [Homo sapiens] >sp|G3834617|G3834617 HOMER-2A. Length = 343	gi|3834617	3	554	96	97	HPWCS14
52	828544			277	474			HPWDE02
53	828546			1	1302			HPWBZ53
54	828550			61	147			HPWBR41

55	828551			61	585			HPWCG88
56	828553	prostate- specific membrane antigen [Homo sapiens] >pir|A56881|A56881 prostate-specific membrane antigen - human	gi|190664	2	655	95	95	HPWCG57
57	828557	NF-IL6-beta protein [Homo sapiens] >pir|A40225|A40225 transcription activator NF-IL6 beta - human Length = 269	gi|189176	3	359	100	100	HPTVR29
58	828560	T-cell receptor (V-J-C) precursor [Homo sapiens] >pir|A26659|A26659 T-cell receptor gamma-1 chain C region - human {SUB 138-310} >gi|339080 T cell receptor gamma chain [Homo sapiens] {SUB 139-310} >gi|339089 T-cell receptor gamma-chain constant region [Ho	gi|339400	381	683	100	100	HPWAY42
59	828561	zinc finger protein [Homo sapiens] >pir|S47071|S47071 finger protein HZF3, Krueppel-related - human (fragment)	gi|498725	1	204	96	96	HPWBS62
60	828565			3	962			HPWAZ16
61	828566			1214	1423			HPWAJ41
62	828567			204	440			HPRTP24
63	828568	thyroid receptor interactor [Homo sapiens] Length = 286	gi|703112	2	475	97	100	HPRSB55
64	828569	envelope protein [Woodchuck hepatitis B virus] >pir|A03708|SAVLC2 large surface antigen - woodchuck hepatitis virus (clone 2) Length = 431	gi|336133	204	395	38	47	HPWBR81
65	828570			380	580			HPRTH40
66	828571	DY3.6 [Caenorhabditis elegans] >sp|O45323|O45323 DY3.6 PROTEIN. Length = 379	gnl|PID|e1345081	2	670	27	61	HPRTP80
67	828574	rTSbeta [Homo sapiens] >sp|Q15407|Q15407 RTSBETA. Length = 416	gnl|PID|e189422	3	458	89	89	HPRTS71
68	828575			3	209			HPRTI65

69	828577			135	395			HPRTQ68
70	828578	phospholipase A2 [unidentified] >gi|190887 synovial phospholipase A-2 [Homo sapiens] >gi|190889 synovial phospholipase A-2 (EC 3.1.1.4) [Homo sapiens] >pir|A32862|PSHUYF phospholipase A2 (EC 3.1.1.4) precursor, synovial fluid - human >sp|P14555|PA2M_HUMAN	gi|833246	136	627	89	89	HPFCL59
71	828580			2	340			HPRCS86
72	828581			103	339			HPRSB02
73	828583			258	419			HPRTL26
74	828585	HOXB13 [Homo sapiens] Length = 284	gi|1764090	1	285	100	100	HPRCN60
75	828587	(AF043431) retinoblastoma-interacting protein [Homo sapiens] >sp|O75371|O75371 RETINOBLASTOMA-INTERACTING PROTEIN. Length = 897	gi|3452281	139	534	100	100	HPRCF61
76	828590			120	248			HPRCE51
77	828592	breakpoint cluster region protein [Homo sapiens] >sp|Q12844|Q12844 BREAKPOINT CLUSTER REGION PROTEIN (FRAGMENT). Length = 889	gi|487346	48	611	98	98	HPRCF63
78	828593	XP-G factor [Homo sapiens] >pir|S35993|S35993 DNA repair protein XPGC - human >sp|G303059|G303059 XPGC=DNA REPAIR PROTEIN RAD2 HOMOLOG. {SUB 1166-1186} Length = 118	gi|298111	1	1272	87	87	HPRTJ39
79	828594			84	353			HPRCM59
80	828596	homeobox protein [Homo sapiens] >pir|S19010|S19010 homeotic protein PBX3a - human >sp|P40426|PBX3_HUMAN PRE-B-CELL LEUKEMIA TRANSCRIPTION FACTOR-3 (HOMEOBOX PROTEIN PBX3).	gi|35315	1	213	93	93	HPRCH15

Length = 434

81	828597	(AL031532) yeast gtr2 homolog, novel small GTPase subfamily protein [Schizosaccharomyces pombe] >sp|O74544|O74544 YEAST GTR2 HOMOLOG, NOVEL SMALL GTPASE SUBFAMILY PROTEIN. Length = 31	gnl|PID|e1319429	1	903	70	85	HPRBB67
82	828598			1	108			HPRAX93
83	828601			2	520			HPRTJ75
84	828605			383	601			HPRAY38
85	828608	acid phosphatase [Homo sapiens] Length = 386	gi|189619	21	533	95	96	HPRBF14
86	828609	prostate- specific membrane antigen [Homo sapiens] >pir|A56881|A56881 prostate-specific membrane antigen - human	gi|190664	186	899	100	100	HPRBH58
87	828610	seminal plasma protein precursor [Homo sapiens] >gi|514372 beta-microseminoprotein [Homo sapiens] >gi|825707 prostatic secretory protein (PSP-94) [Homo sapiens]	gi|338415	3	398	100	100	HPRTJ08
88	828617			3	350			HPRAD26
89	828620	prostatic acid phosphatase [Homo sapiens] >gi|189621 acid phosphatase [Homo sapiens] >gi|515997 prostatic acid phosphatase [Homo sapiens]	gi|189613	3	650	94	94	HPRBF16
90	828621			4	126			HPRAG37
91	828622			28	156			HPRAQ51
92	828623			125	313			HPRAG59
93	828625			87	275			HPRAT22
94	828632			68	406			HPQBV63
95	828635			916	1344			HPMGE79

96	828637	(AC005600) PKD1 [Homo sapiens] >sp|O75276|O75276 PKD1 (FRAGMENT). Length = 1339	gi|3522923	1	366	70	71	HPOAB53
97	828639			72	158			HPMDB85
98	828645			2	313			HPJCK50
99	828648	(AF059569) actin binding protein MAYVEN [Homo sapiens] >sp|G3789797|G3789797 ACTIN BINDING PROTEIN MAYVEN. Length = 593	gi|3789797	210	677	32	48	HPJBV55
100	828649	neuropeptide Y [Homo sapiens] >gi|189282 neuropeptide Y [Homo sapiens] >gi|2992498 (AC004485) neuropeptide Y precursor [Homo sapiens]	gi|189274	121	375	100	100	HPWBU56
101	828651	similar to ATPases associated with various cellular activities (AAA);	gnl|PID|e1351769	41	742	51	69	HPJDA05
102	828652			1	189			HPJCY65
103	828655			60	251			HPJBW32
104	828657	(AF061283) neuronal protein 4.1 [Mus musculus] >sp|G3790545|G3790545 NEURONAL PROTEIN 4.1. Length = 879	gi|3790545	38	328	45	67	HPJBD30
105	828660			103	231			HPJCL80
106	828663	calnexin [Homo sapiens] >gi|186523 calnexin [Homo sapiens] >pir|A46673|A46673 calnexin precursor - human >sp|P27824|CALX_HUMAN CALNEXIN PRECURSOR (MAJOR HISTOCOMPATIBILITY COMPLEX CLASS I ANTIGEN-BINDING PROTEIN P88) (P90) (IP90). Length = 592	gi|306481	41	703	87	87	HPJCT42
107	828666			1	246			HPJBI71
108	828668			61	315			HPJBK31
109	828669			1	225			HPJBU60
110	828670			222	350			HPICC36

111	828671	(AJ005866) Sqv-7-like protein [Homo sapiens] >sp|E1360006|E1360006 SQV-7-LIKE PROTEIN (FRAGMENT). Length = 261	gnl|PID|e1360006	3	1025	89	90	HPJAD23
112	828672			1	255			HPICD86
113	828675	MCM4 [Homo sapiens] >sp|G2754697|G2754697 MCM4 (FRAGMENT). Length = 712	gi|2754697	2	2173	99	99	HPJBZ66
114	828677			113	268			HPICC05
115	828678	SNAP43 [Homo sapiens] >gi|1174203 PSE-binding factor PTF gamma subunit [Homo sapiens] >pir|JC6081|JC6081 proximal sequence element-binding transcription factor gamma chain - human >sp|Q16533|Q16533 PSE-BINDING FACTOR PTF GAMMA SUBUNIT. Length = 368	gi|623244	2	664	98	98	HPJAA76
116	828679			142	318			HPJAC93
117	828680	DNA primase (subunit p48) [Homo sapiens] >pir|S45630|S45630 DNA primase chain p48 - human >sp|P49642|PRI1_HUMAN DNA PRIMASE SMALL SUBUNIT (EC 2.7.7.-) (DNA PRIMASE 49 KD SUBUNIT) (P49). >gi|2353692 DNA primase 1 [Homo sapiens] {SUB 97-146} Length = 420	gi|510406	74	652	100	100	HPICG94
118	828681			3	167			HPJAA30
119	828682			3	617			HPIBM51
120	828683			54	329			HPIBR22
121	828686	(AF006010) progestin induced protein [Homo sapiens] >sp|G4101695|G4101695 PROGESTIN INDUCED PROTEIN. Length = 2796	gi|4101695	2	886	95	97	HPIBQ56
122	828687			27	131			HPIBS12

123	828688	CCAAT-box DNA binding protein subunit NF-YB [Homo sapiens] >sp|P25208|CBFA_HUMAN CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).	gi|189199	128	757	100	100	HPJAA20
124	828689	creatine kinase [Homo sapiens] >pir|A31431|A30789 creatine kinase (EC 2.7.3.2) precursor, mitochondrial - human >sp|P12532|KCRU_HUMAN CREATINE KINASE, UBIQUITOUS MITOCHONDRIAL PRECURSOR (EC 2.7.3.2) (U- MTCK) (MIA-CK) (ACIDIC-TYPE MITOCHONDRIAL CREATINE K	gi|180590	227	1222	84	84	HPICC13
125	828692	(AJ223301) aralkyl acyl-CoA:amino acid N-acyltransferase [Bos taurus] >gi|2865607 (AF045032) aralkyl acyl-CoA:amino acid N-acyltransferase [Bos taurus] >sp|O46686|O46686 ARALKYL ACYL-COA:AMINO ACID N-ACYLTRANSFERASE (EC 2.3.1.13) (GLYCINE N-ACYLTRANSFERAS	gnl|PID|e1248977	278	1000	49	70	HPIBO30
126	828693	dJ14O9.2 (Melanoma-Associated Antigen MAGE LIKE) [Homo sapiens] >sp|O76058|O76058 DJ14O9.2 (MELANOMA-ASSOCIATED ANTIGEN MAGE LIKE). Length = 606	gnl|PID|e1311294	1	426	45	69	HPIBL27
127	828694			1	333			HPIBY69
128	828696			171	347			HPIBA33

129	828697	kynurenine/alpha-aminoadipate aminotransferase [Rattus norvegicus] >sp|Q64602|Q64602 KYNURENINE/ALPHA-AMINOADIPATE AMINOTRANSFERASE (EC 2.6.1.7) (KYNURENINE--OXOGLUTARATE AMINOTRANSFERASE) (KYNURENINE AMINOTRANSFERASE). Length = 425	gi|1050752	258	422	61	72	HPICB03	
130	828699			3	1109			HPIBL48	
131	828702	prostate- specific membrane antigen [Homo sapiens] >pir|A56881|A56881 prostate-specific membrane antigen - human >bbs|164191 prostate-specific membrane antigen.	gi|190664	118	744	76	78	HPIAZ02	
132	828703			285	689			HPIBB96	
133	828704	put. DNA topoisomerase I (AA 1-864) [Escherichia coli] >gnl|PID|d1015527 DNA topoisomerase I (EC 5.99.1.2) (w-protein) (Relaxing enzyme) (Untwisting enzyme) (Swivelase). [Escherichia coli]	gi|415338	2	406	98	98	HPIBH30	
134	828706	mitotic centromere-associated kinesin [Homo sapiens] >sp|Q99661|Q99661 MITOTIC CENTROMERE-ASSOCIATED KINESIN. Length = 725	gi|1695882	559	1788	98	98	HPIBJ11	
135	828708			2	589			HPIAW81	
136	828711			1	93			HPIAZ32	
137	828712			49	309			HPIAU16	
138	828713			142	396			HPIAV37	
139	828714			68	1849			HPIAV20	
140	828715			174	356			HPIAS34	
141	828718	ipa-6d gene product [Bacillus subtilis] >gnl|PID|e1186348 alternate gene name: ipa-6d; similar to quinone biosynthesis [Bacillus subtilis]	gi|413930	403	1308	35	57	HPIAL41	

142	828723	UDP glucuronosyltransferase precursor [Homo sapiens] >pir|A48633|A48633 dihydrotestosterone/androstanediol UDP-glucuronosyltransferase isoform 3, udpgth-3 - human	gi|475759	3	206	97	100	HPIAL34
143	828726	hydrophobic membrane-bound protein [Escherichia coli] >gi|1147818 part of a molybdenum periplasmic binding protein dependent transport system [Escherichia coli] >gi|973215 ModB [Escherichia coli]	gi|504499	1	255	98	98	HPIAS69
144	828728	(AF044954) NADH:ubiquinone oxidoreductase PDSW subunit [Homo sapiens] >gi|4165091 (AF088991) NADH-ubiquinone oxidoreductase PDSW subunit [Homo sapiens] Length = 172	gi|4164442	1	498	84	86	HPIAS40
145	828730	MAK11 protein [Saccharomyces cerevisiae] >gi|486013 ORF YKL021c [Saccharomyces cerevisiae] >pir|A29938|A29938 MAK11 protein - yeast (Saccharomyces cerevisiae) >sp|P20484|MK11_YEAST MAK11 PROTEIN. Length = 468	gi|171877	394	1569	34	64	HPHAF82
146	828732	rab geranylgeranyl transferase [Homo sapiens] >pir|JC5538|JC5538 Rab geranylgeranyl transferase (EC 2.5.1.-) alpha chain - human >sp|E1256376|E1256376 RAB GERANYLGERANYL TRANSFERASE. Length = 567	gnl|PID|e1256376	155	868	97	97	HPIAN07
147	828733			202	438			HPIAK81
148	828735	(AF006265) cancer associated surface antigen [Homo sapiens] >gnl|PID|d1023440 (AB007619) EBAG9 [Homo sapiens] >sp|O00559|O00559 CANCER ASSOCIATED SURFACE ANTIGEN. Length = 213	gi|2213934	369	1139	90	90	HPIAE30

149	828736			1	132			HPFEA11
150	828739			60	347			HPIAA46
151	828740			2	394			HPIAC69
152	828742			2	475			HPHAB61
153	828748	glandular kallikrein precursor [Homo sapiens] >pir|A29586|A29586 tissue kallikrein (EC 3.4.21.35) hGK-1 precursor - human >sp|P20151|KLK2_HUMAN GLANDULAR KALLIKREIN 2 PRECURSOR (EC 3.4.21.35) (TISSUE KALLIKREIN) (PROSTATE) (HGK-1). Length = 261	gi|386842	3	707	95	96	HPEAB20
154	828749	serine/threonine kinase [Rattus norvegicus] >sp|O08678|O08678 SERINE/THREONINE KINASE. Length = 793	gnl|PID|e290956	443	826	94	99	HPIAA79
155	828752	androgen regulated homeobox protein [Homo sapiens] >sp|Q99801|HK31_HUMAN HOMEOBOX PROTEIN NKX-3.1. Length = 234	gi|1732378	1051	1692	99	99	HPIAA91
156	828753			2	187			HPFEA08
157	828754			423	566			HPFDD83
158	828757			2	409			HPFDI21
159	828761			3	113			HPFDE61
160	828762			3	317			HPFDE33
161	828764	cytochrome c oxidase subunit VIc preprotein [Homo sapiens] >gi|3859868 (AF067637) cytochrome c oxidase subunit VIc [Homo sapiens]	gnl|PID|e223120	51	329	100	100	HPMSH48
162	828765			3	80			HPFDB49
163	828766			90	242			HPFDT61
164	828767			797	937			HPWDK71
165	828768			1109	1324			HPFDD04
166	828770			156	392			HPFDF79

167	828771	(AF001629) WASP interactor protein [Homo sapiens] >sp|G4100621|G4100621 WASP INTERACTOR PROTEIN (FRAGMENT). Length = 328	gi|4100621	1	273	55	61	HPFDS50
168	828772			200	340			HPFDT28
169	828773			115	348			HPFDE85
170	828775			23	208			HPFCR19
171	828776			3	134			HPFCY40
172	828777			131	919			HPFDM39
173	828778			2	121			HPFCZ89
174	828780			46	420			HPFDA70
175	828781			408	734			HPFCP06
176	828782			61	186			HPFDI40
177	828783	relaxin [Homo sapiens] >gi|490063 H1-relaxin [Homo sapiens] >gi|412167 relaxin [Homo sapiens] >gi|512431 preprorelaxin [Homo sapiens] >gi|35933 prepro-relaxin H1 [Homo sapiens]	gi|490056	68	253	70	70	HPFCH80
178	828784			82	321			HPFCT79
179	828785			32	250			HPFCX77
180	828786			302	532			HPFCT31
181	828788			341	538			HPFCI59
182	828790			195	317			HPFCT53
183	828791			6	140			HPFCI14
184	828792			121	801			HPFCC91
185	828794			1219	1440			HPFCJ56
186	828797			128	259			HPFCC42
187	828798			237	350			HPFCI76
188	828799			113	322			HPFAA95
189	828801			90	239			HPEAG41
190	828802			165	392			HPFCL26

191	828803	(AB022017) AMP-activated protein kinase alpha-1 [Homo sapiens] >sp|D1037533|D1037533 AMP-ACTIVATED PROTEIN KINASE ALPHA-1. >gnl|PID|e315274 AMP-activated protein kinase alpha-1 [Homo sapiens] {SUB 294-550}	gnl|PID|d1037533	96	458	83	83	HPITBA83
192	828804			98	286			HPEAC32
193	828805			166	303			HPFCF17
194	828807			1	195			HPFCF96
195	828809			147	236			HPEAC52
196	828810			1	153			HPEBT31
197	828811			283	426			HPFAA06
198	828817			2	160			HPCAC47
199	828818			1	258			HPEAA76
200	828819			345	623			HPEBG44
201	828820			314	502			HPEAB80
202	828821			246	416			HPCAF64
203	828823	spore coat protein SP87 [Dictyostelium discoideum] Length = 677	gi|915203	267	875	44	61	HPEAB79
204	828824			458	643			HPCAC56
205	828825			132	446			HPDDY72
206	828826			2	730			HPCAN60
207	828829			499	672			HPCAO54
208	828830	Arnt [Homo sapiens] >pir|I59550|I59550 Arnt - human >sp|P27540|ARNT_HUMAN ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR (ARNT PROTEIN) (DIOXIN RECEPTOR, NUCLEAR TRANSLOCATOR) (HYPOXIA-INDUCIBLE FACTOR 1 BETA) (HIF-1 BETA). Length = 789	gi|179004	1	219	90	92	HPCAA27
209	828833			42	278			HPCAB16
210	828835			61	474			HOUDC43

211	828838	chordin [Xenopus laevis] >pir|A55195|A55195 chordin precursor - African clawed frog >sp|Q91713|CHRD_XENLA CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR). Length = 941	gi|603945	2	1468	43	56	HPCAO32
212	828840			536	679			HOVCJ65
213	828845			69	212			HOSDG69
214	828846			3	1034			HSPBQ12
215	828847			36	395			HPEAA46
216	828849	(AF041474) BAF53a [Homo sapiens] >sp|G4001803|G4001803 BAF53A. Length = 429	gi|4001803	62	1468	100	100	HOVCJ86
217	828850	putative [Homo sapiens] >pir|A49364|A49364 59 protein, brain - human (fragment) >sp|Q09019|DMR9_HUMAN DMR-N9 PROTEIN (PROTEIN 59) (FRAGMENT). Length = 553	gi|306712	2	283	97	97	HOUCP33
218	828852			96	437			HOSAZ63
219	828853	(AC004449) R33683_3 [Homo sapiens] >sp|O60372|O60372 R33683_3 (FRAGMENT). Length = 103	gi|2979531	1	465	40	62	HOSAV36
220	828857	uridine kinase [Mus musculus] Length = 260	gi|471981	3	1013	74	88	HQQBM19
221	828861			2	991			HPEAE55
222	828866	enhancer of filmentation 1 [Homo sapiens] >gi|1490787 Crk-associated substrate related protein Cas-L [Homo sapiens] >sp|Q14511|Q14511 ENHANCER OF FILMENTATION 1. Length = 834	gi|1280212	143	637	100	100	HOHBF14
223	828872	pericentriol material 1 [Homo sapiens] >pir|A54103|A54103 centrosome autoantigen PCM-1 - human >sp|Q15154|Q15154	gi|450277	295	879	93	94	HOHAL47

PERICENTRIOL MATERIAL 1. Length = 2024

224	828874	histone H1(0) (aa 1-194) [Homo sapiens] >pir|A24850|HSHU10 histone H1-0 - human >sp|P07305|H10_HUMAN HISTONE H1' (H1.0) (H1(0)). {SUB 2-194} Length = 194	gi|32107	3	902	82	82	HOGBL72
225	828875	myosin VI [Homo sapiens] >sp|G2304981|G2304981 MYOSIN VI. Length = 1262	gi|2304981	1	450	99	99	HOGCC24
226	828877	75 kDa subunit NADH dehydrogenase precursor [Homo sapiens] >pir|S17854|S17854 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 75K chain precursor - human	gi|38079	24	275	95	97	HOFMJ67
227	828878	S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) old gene name 'AMD' [Homo sapiens] >pir|A31786|DCHUDM adenosylmethionine decarboxylase (EC 4.1.1.50) precursor - human	gi|178518	282	1325	95	95	HOGCC89
228	828879			2	271			HOEJH17
229	828881			139	969			HOGAF39
230	828885	product possesses binding site dependent transcriptional suppressing activity [Homo sapiens] >pir|A44351|A44351 transcription repressor E4BP4 - human >sp|Q14211|Q14211 E4BP4 GENE. Length = 462	gi|30956	173	1639	94	95	HOEEC58
231	828886			82	228			HODGT65
232	828887	ZNF127-Xp [Homo sapiens] >sp|Q13434|Q13434 ZNF127-XP. Length = 485	gi|1304599	2	1327	56	76	HOECN41

233	828889	neurofibromin [Homo sapiens] >sp|P21359|NF1_HUMAN NEUROFIBROMIN (NEUROFIBROMATOSIS-RELATED PROTEIN NF-1). >gi|736765 neurofibromatosis 1 [Homo sapiens] {SUB 751-1611} >gi|189161 neurofibromatosis protein type 1 [Homo sapiens] {SUB 1168-1566}	gi|292354	265	690	89	89	HODAQ30
234	828891	FAST kinase [Homo sapiens] >pir|I37386|I37386 FAST kinase - human >sp|Q14296|Q14296 FAST KINASE. Length = 549	gi|1006659	84	1238	100	100	HODDG78
235	828899			3	344			HNWAA42
236	828907			3	566			HNTSS75
237	828911			1217	1501			HNTMC68
238	828914	MAP KINASE-ACTIVATED PROTEIN KINASE 2 (EC 2.7.1.-) (MAPK-ACTIVATED PROTEIN KINASE 2) (MAPKAP KINASE 2) (MAPKAPK-2). Length = 400	sp|P49137|MKK2_HUMAN	586	1176	98	99	HNTRL23
239	828917	zinc finger protein 7 (ZFP7) [Homo sapiens] >pir|A34612|A34612 zinc finger protein ZNF7 - human Length = 686	gi|340446	790	1536	57	70	HNTCR38
240	828921	RNA helicase [Homo sapiens] >pir|S71758|S71758 DEAD box protein MrDb, Myc-regulated - human >sp|Q92732|Q92732 RNA HELICASE. Length = 610	gnl|PID|e254454	123	1253	90	90	HNTRO07
241	828922			138	1403			HNTAB76
242	828924	(AE000180) biotin synthesis, sulfur insertion? [Escherichia coli] >gi|490219 BIOB gene product [Escherichia coli] >gnl|PID|e305036 BIOTIN SYNTHASE [Escherichia coli] >pir|JC2517|SYECBB biotin synthetase (EC 2.8.1.-) - Escherichia coli	gi|1786992	1	78	95	95	HNHAG14

>sp|P12996|BIOB_ECOL

243	828925			376	426			HNGKM39
244	828926			28	522			HNTBH70
245	828928			1	330			HNGNK23
246	828930	casein kinase I-alpha [Homo sapiens] >pir|A57011|A57011 casein kinase I-alpha - human Length = 337	gi|852055	412	1467	89	91	HNFJJ04
247	828935	(AL021366) cICK0721Q.3 (Kinesin related protein) [Homo sapiens] >sp|O60887|O60887 CICK0721Q.3 (KINESIN RELATED PROTEIN). >gnl|PID|e1332987 (AJ010479) kinesin-like protein [Homo sapiens] {SUB 1-274} Length = 673	gnl|PID|e1330109	2	1447	86	86	HNTRL26
248	828937	apurinic/apyrimidinic endonuclease [Homo sapiens] >gi|183780 apurinic/apyrimidinic endonuclease [Homo sapiens] >gi|32022 AP endonuclease 1 [Homo sapiens] >bbs|111437 Ref-1=redox factor [human, Peptide, 318 aa] [Homo sapiens] >pir|S23550|S23550 DNA-(apurin	gi|178747	124	1158	95	95	HNTNM15
249	828940	pol polyprotein - Moloney murine leukemia virus (strain 3-1R) (fragment) Length = 559	pir|A46311|A46311	1399	1806	58	71	HNGGG72
250	828942			3	386			HNFHK65

251	828943	rapamycin binding protein [Homo sapiens] >gi|182644 FK506-binding protein 25 [Homo sapiens] >prf|JQ1522|JQ1522 peptidylprolyl isomerase (EC 5.2.1.8) FKBP3 - human >sp|Q00688|FKB3_HUMAN RAPAMYCIN-SELECTIVE 25 KD IMMUNOPHILIN (FKBP25) (PEPTIDYL-PROLYL CIS-T	gi|182626	3	710	100	100	HMWHSH8
252	828946	hepatitis delta antigen interacting protein A [Homo sapiens] >sp|Q15834|Q15834 HEPATITIS DELTA ANTIGEN INTERACTING PROTEIN A. Length = 202	gi|1488314	118	729	66	66	HMWHE39
253	828947			199	396			HMWHM20
254	828956	(AJ029071) p52 pro-apoptotic protein [Gallus gallus] Length = 465	gi|2599492	470	1384	74	86	HMWGG82
255	828958			1	306			HMWHS21
256	828965	pterin-4a-carbinolamine dehydratase [Homo sapiens] >gi|848987 pterin-4a-carbinolamine dehydratase [Homo sapiens] >gnl|PID|e1292435 (AJ005542) dimerization cofactor of HNF1; pterin-4a-carbinolamin dehydratase [Rattus norvegicus] >gnl|PID|e1292435 (AJ005542	gi|848985	2	370	100	100	HMWED17
257	828969	Rat-BP (Rat-binding protein 1) [Homo sapiens] Length = 200	gnl|PID|d1007847	2	742	91	91	HMWFM25
258	828971			574	753			HMVAJ71
259	828973	similar to leucyl-tRNA synthetase;	gnl|PID|e1344085	85	678	74	88	HMUBQ39
260	828980	acidic 82 kDa protein [Homo sapiens] >pir|G01522|G01522 acidic 82 kDa protein - human >sp|Q12987|Q12987 ACIDIC 82 KDA PROTEIN. Length = 736	gi|558458	3	524	88	88	HMTME58

261	828984	high mobility group box [Homo sapiens] >pir|A41976|A41976 structure-specific recognition protein, SSRP1 - human Length = 709	gi|184242	322	2388	97	97	HMUAQ01
262	828985			734	928			HMSGL25
263	828988	Similarity to Yeast MSP1 protein (TAT-binding homolog 4) (SW:MSP1_YEAST) [Caenorhabditis elegans] >sp|P54815|MSP1_CAEEL MSP1 PROTEIN HOMOLOG. Length = 357	gnl|PID|e1347884	1	1137	79	88	HMUBL18
264	828993			78	308			HMTMB67
265	828995			653	1567			HMSIV02
266	829000			296	478			HMMBW26
267	829005			1	531			HMQA148
268	829009	GTP-binding protein [Homo sapiens] >sp|O43824|O43824 GTP-BINDING PROTEIN. Length = 442	gnl|PID|e1227622	64	927	88	88	HMQA169
269	829010	(AF035537) DNA polymerase zeta [Homo sapiens] Length = 3052	gi|2665742	282	1262	93	93	HMSGH89
270	829012	ribophorin II precursor - human Length = 631	pir|B26168|B26168	161	2188	94	95	HMSJH16
271	829013			1339	1506			HMIAX25
272	829019			41	223			HMIAJ48
273	829020	similar to WD domain, G-beta repeats (2 domains);	gnl|PID|e1345001	21	800	60	77	HMELR71
274	829021			356	640			HMIAJ26
275	829026	RIZ [Homo sapiens] >sp|Q13029|Q13029 ZINC FINGER PROTEIN RIZ. >pir|I38902|I38902 retinoblastoma-binding protein RIZ - human {SUB 3-1721} Length = 1721	gi|3645905	89	1183	87	87	HMELM45

276	829030	chaperonin-like protein [Homo sapiens] >pir|S48087|S48087 t-complex-type molecular chaperone CCT6 - human >gi|184462 chaperonin-like protein [Homo sapiens] {SUB 143-531} Length = 531	gi|517065	1	1674	95	95	HMICQ08
277	829035	(AF082516) I-1 receptor candidate protein [Homo sapiens] >sp|G3462807|G3462807 I-1 RECEPTOR CANDIDATE PROTEIN. >gi|3493225 (AF058290) imidazoline receptor antisera-selected protein [Homo sapiens] {SUB 469-1063} Length = 1504	gi|3462807	2	679	98	98	HMEFK17
278	829041	pyrroline-5-carboxylate reductase [Homo sapiens] >pir|A41770|A41770 pyrroline-5-carboxylate reductase (EC 1.5.1.2) - human >sp|P32322|PROC_HUMAN PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE). Length = 319	gi|189498	268	1032	99	100	HMEIQ04
279	829045			2	1771			HMEKR35
280	829048			115	1467			HMEJC44
281	829051			2	256			HMEBI38
282	829052			795	1154			HMHBD67
283	829057			116	799			HMEAF61
284	829058			3	536			HMEER28
285	829059			310	501			HMDAQ69
286	829061			3	101			HMCFX82
287	829062	(AF095791) TACC2 protein [Homo sapiens] >sp|G3777596|G3777596 TACC2 PROTEIN (FRAGMENT). Length = 653	gi|3777596	1417	2622	50	71	HMCGK90
288	829063	kinesin-like DNA binding protein KID - human Length = 665	pir|S62328|S62328	58	1437	83	84	HMEFI72
289	829064			2	718			HMADG63

290	829066	37KD protein, similar to YI22-ECOLI [Escherichia coli] >sp|Q47535|Q47535 37KD PROTEIN, SIMILAR TO YI22-ECOLI. Length = 424	gnl|PID|d1013520	600	1427	98	98	HMAHX38
291	829068	(AF037204) RING zinc finger protein [Homo sapiens] >gi|3387925 (AF070558) RING zinc finger protein RZF [Homo sapiens] >sp|O43567|O43567 RING ZINC FINGER PROTEIN. Length = 381	gi|2746333	432	1319	84	84	HMSH92
292	829069			1	207			HLYET39
293	829074			1	1269			HLYDE91
294	829077			181	873			HLYFD84
295	829078	topoisomerase I [Homo sapiens] >gi|473581 DNA topoisomerase I [Homo sapiens] {SUB 5-765} >gnl|PID|e1312191 (AL022394) dJ511B24.1 (Topoisomerase I) [Homo sapiens] {SUB 437-765} Length = 765	gi|339804	2	907	69	78	HLYCP31
296	829079			194	382			HLYBT93
297	829085	putative ATP/GTP-binding protein [Homo sapiens] >sp|Q92989|Q92989 PUTATIVE ATP/GTP-BINDING PROTEIN. Length = 425	gi|1644402	67	783	93	93	HMCEJ41
298	829093	26S proteasome-associated pad1 homolog [Homo sapiens] >sp|O00487|O00487 26S PROTEASOME-ASSOCIATED PAD1 HOMOLOG. Length = 310	gi|1923256	307	1251	100	100	HLYAN96
299	829099	alpha-L-fucosidase precursor (EC 3.2.1.5) [Homo sapiens] >pir|A33427|HWHUFA alpha-L-fucosidase (EC 3.2.1.51) I precursor, tissue - human >gnl|PID|e34843 alpha-L-fucosidase [Homo sapiens] {SUB 357-393} Length = 461	gi|178409	2	850	96	96	HLTDK55
300	829101	protein tyrosine phosphatase [Homo sapiens] Length = 415	gi|804750	3	542	100	100	HLYAP23

301	829102	!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! Length = 593	sp|P39194|ALU7_HUMAN	3	59	84	94	HLTEO83
302	829103			265	663			HLWAC24
303	829104			316	525			HLWAX30
304	829109			3	155			HLTCF21
305	829111			1	333			HLTGS92
306	829115			2	670			HLTHA72
307	829116			104	265			HLQDA07
308	829119			144	374			HLMCG37
309	829120			611	910			HLTGP61
310	829121			558	698			HLQCN32
311	829123	aldehyde oxidase [Homo sapiens] >pir|A49634|A49634 aldehyde oxidase (EC 1.2.3.1) - human >sp|Q06278|ADO_HUMAN ALDEHYDE OXIDASE (EC 1.2.3.1). Length = 1338	gi|438656	7	585	99	99	HLQDA57
312	829126			2	154			HLQCX53
313	829135	beta-D-galactosidase precursor (EC 3.2.1.23) [Homo sapiens] >gi|179423 beta-galactosidase precursor (EC 3.2.1.23) [Homo sapiens] >pir|A32688|A32611 beta-galactosidase (EC 3.2.1.23) precursor - human	gi|179401	3	2090	98	98	HLQAM57
314	829136	(AJ005458) protein Phosphatase 2C beta [Bos taurus] >sp|O62830|O62830 PROTEIN PHOSPHATASE 2C BETA (EC 3.1.3.16). Length = 387	gnl|PID|e1287413	55	1254	95	96	HLTHS28

315	829138	cytochrome b5 [Homo sapiens] >pir|A28936|CBHU5 cytochrome b5, microsomal form - human >sp|P00167|CYB5_HUMAN CYTOCHROME B5. {SUB 2-134} >gi|181229 cytochrome b5 [Homo sapiens] {SUB 87-134} Length = 134	gi|181227	35	499	89	89	HLHTN31
316	829142	(AF016509) oxidoreductase [Homo sapiens] >sp|O14756|O14756 OXIDOREDUCTASE. Length = 317	gi|2338748	2	1135	99	99	HLIBJ28
317	829148			55	279			HLHDP51
318	829149	protein kinase C iota [Homo sapiens] >gi|598225 protein kinase C iota [Homo sapiens] >pir|A49509|A49509 protein kinase C (EC 2.7.1.-) iota - human	gi|432274	1	783	99	100	HLICD11
319	829156	ORF YDL063c [Saccharomyces cerevisiae] >pir|S67598|S67598 probable membrane protein YDL063c - yeast (Saccharomyces cerevisiae)	gnl|PID|e253210	3	347	82	83	HLHCD19
320	829162	(AF019767) zinc finger protein [Homo sapiens] >sp|O75312|O75312 ZINC FINGER PROTEIN. Length = 459	gi|3510462	3	890	88	89	HLGDA89
321	829170			2	160			HLDBY56
322	829177	complement factor B [Homo sapiens] >gi|2347133 (AF019413) complement factor B [Homo sapiens] >gi|553536 MHC factor B [Homo sapiens] {SUB 339-509} Length = 764	gi|291922	1	600	86	87	HLDBN31
323	829179			518	847			HL2AG36

324	829184	CDC2 polypeptide (CDC2) (AA 1-297) [Homo sapiens] >gi|29841 CDC2 protein (AA 1-297) [Homo sapiens] >pir|A29539|A29539 protein kinase (EC 2.7.1.37) cdc2 - human >sp|P06493|CC2_HUMAN CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (P34 PROTEIN KINASE)	gi|29839	553	1005	98	98	HL1BD94
325	829185			77	295			HL2AH06
326	829188	M-phase phosphoprotein 4 [Homo sapiens] >sp|Q99545|Q99545 M-PHASE PHOSPHOPROTEIN 4 (FRAGMENT). Length = 611	gnl|PID|e248491	282	1238	92	92	HLAAB63
327	829190	(AF038869) eukaryotic initiation factor 4E-binding protein 3 [Homo sapiens] >sp|O60516|O60516 EUKARYOTIC INITIATION FACTOR 4E-BINDING PROTEIN 3. Length = 100	gi|3169393	3	359	87	87	HL2AG38
328	829193	protein kinase [Homo sapiens] >pir|S34130|S34130 serine/threonine-specific protein kinase PLK (EC 2.7.1.-) - human >sp|P53350|PLK1_HUMAN SERINE/THREONINE-PROTEIN KINASE PLK (EC 2.7.1.-) (PLK-1) (SERINE- THREONINE PROTEIN KINASE 13) (STPK13). Length = 603	gi|312998	2	988	94	94	HL4AF38
329	829196			1	432			HL1AR10
330	829197	TAK1 binding protein [Homo sapiens] >sp|Q15750|Q15750 TAK1 BINDING PROTEIN. Length = 504	gi|1401126	1	252	75	76	HL1BM07
331	829202	(AF060502) peroxisome assembly protein PEX10 [Homo sapiens] >sp|O60683|PEXA_HUMAN PEROXISOME ASSEMBLY PROTEIN PEX10 (PEROXIN-10). Length = 326	gi|3170653	97	465	92	94	HL1AY04

332	829203			1	258			HL1AL88
333	829209			127	342			HL2AF80
334	829210			148	315			HL1AG80
335	829214	cyclin G2 [Homo sapiens] >gi|1236915 cyclin G2 [Homo sapiens] >sp|Q16589|Q16589 CYCLIN G2. Length = 344	gi|1236235	2	484	74	74	HKMSB51
336	829215			29	175			HL1AG81
337	829219			24	290			HL1AG22
338	829220			68	664			HKMMC06
339	829222	(AF016371) U-snRNP-associated cyclophilin [Homo sapiens] >gi|3647230 (AF036331) cyclophilin [Homo sapiens] >sp|O43447|O43447 U-SNRNP-ASSOCIATED CYCLOPHILIN (EC 5.2.1.8). Length = 177	gi|2708309	1	549	100	100	HKGBU67
340	829223			2	187			HL1AC64
341	829225	probable transposase - human transposable element MER37 >pir|S72486|S72486 putative transposase - human transposon MER37 (fragment) {SUB 177-349} Length = 454	pir|S72481|S72481	1607	1720	80	87	HNEBF88
342	829226	pre-B cell enhancing factor [Homo sapiens] >pir|A55927|A55927 pre-B cell enhancing factor - human >sp|P43490|PBEF_HUMAN PRE-B CELL ENHANCING FACTOR PRECURSOR. Length = 491	gi|404013	186	1730	97	97	HKMMZ30
343	829227			285	548			HK1YE27
344	829231			42	92			HKMME67
345	829232	cyclin A [Homo sapiens] >gi|510604 cyclin A [Homo sapiens] >pir|S08277|S08277 cyclin A - human >sp|P20248|CG2A_HUMAN G2/MITOTIC-SPECIFIC CYCLIN A. Length = 432	gi|30307	2	1546	94	95	HKGDC59
346	829233			123	446			HKGBH49

347	829239			141	782			HKFBA66
348	829240			144	347			HKGAB62
349	829242	palmitoyl-protein thioesterase [Homo sapiens] >gi|1314355 palmitoyl protein thioesterase [Homo sapiens] >gi|2465725 (AF022211) palmitoyl-protein thioesterase [Homo sapiens] >sp|P50897|PPT_HUMAN PALMITOYL-PROTEIN THIOESTERASE PRECURSOR (EC 3.1.2.22) (PALMI	gi|1160967	2	955	100	100	HKHAK14
350	829246			68	424			HKAFK34
351	829250			169	309			HKAJW63
352	829253			158	982			HKAHA61
353	829256	(AF094583) putative HIV-1 infection related protein [Homo sapiens] >sp|G3885931|G3885931 PUTATIVE HIV-1 INFECTION RELATED PROTEIN (FRAGMENT). Length = 129	gi|3885931	1043	1831	89	89	HKAFL67
354	829263	histone H4 [Tigriopus californicus] >gi|297562 histone H4 [Chironomus thummi] >gi|7084 histone H4 gene product [Chironomus thummi] >gi|7440 histone H4 [Drosophila hydei] >gnl|PID|e242831 histone H4 [Drosophila hydei] >gnl|PID|e242923 histone H4 [Drosophil	gi|10616	2	361	98	98	HKADJ19
355	829266	similar to S. cerevisiae longevity-assurance protein 1 (SP:P38703) [Caenorhabditis elegans] >sp|Q17870|Q17870 SIMILAR TO S. CEREVISIAE LONGEVITY-ASSURANCE PROTEIN 1. Length = 362	gi|1123105	115	636	43	58	HKADL80

356	829271	cAMP response element regulatory protein [Homo sapiens] >gnl|PID|d1014939 TAXREB67 protein [Homo sapiens] >pir|A45377|A45377 transcription factor CREB-2 - human >sp|P18848|ATF4_HUMAN CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-4 (DNA-BINDING PROTEIN TAX	gi|181041	261	1118	86	86	HLIAG18
357	829273	unknown [Homo sapiens] >pir|I38891|I38891 hypothetical protein - human (fragment) >sp|Q13021|BENE_HUMAN BENE PROTEIN (FRAGMENT). Length = 148	gi|1000712	1	507	94	94	HKAEP12
358	829274	(AB006202) cytochrome b small subunit of complex II [Homo sapiens] >sp|O14521|DHSD_HUMAN SUCCINATE DEHYDROGENASE [UBIQUINONE] CYTOCHROME B SMALL SUBUNIT PRECURSOR (CYBS) (SUCCINATE-UBIQUINONE REDUCTASE MEMBRANE ANCHOR SUBUNIT). Length = 159	gnl|PID|d1022913	55	546	76	76	HKAPF38
359	829276	Similar to D.melanogaster cadherin-related tumor suppressor [Homo sapiens] >sp|Q92566|Q92566 MYELOBLAST KIAA0279 (FRAGMENT). Length = 2408	gnl|PID|d1014097	272	2422	90	90	HKAC858
360	829279	(AC005620) R33590_2, partial CDS [Homo sapiens] >sp|O75291|O75291 R33590_2, PARTIAL CDS (FRAGMENT). Length = 121	gi|3548790	163	597	95	95	HKAAS81
361	829280			172	375			HJKSB47
362	829283			235	414			HJAAF37
363	829284			2	322			HJMBB19
364	829285			706	912			HKADQ69
365	829287			134	358			HJAAB29
366	829295			81	212			HJACK32

367	829296			352	666			HISAN67
368	829297	mitotic kinase-like protein-1 [Homo sapiens] >pir|S28262|S28262 kinesin-related protein MKLP-1 - human >sp|Q02241|MKLP_HUMAN MITOTIC KINESIN-LIKE PROTEIN-1. Length = 960	gi|34672	1	225	98	98	HJPBA19
369	829298	O-6-methylguanine-DNA methyltransferase [Homo sapiens] >gi|307199 6-O-methylguanine-DNA methyltransferase (EC 2.1.1.63) [Homo sapiens] >gi|34559 O-6-methylguanine-DNA methyltransferase [Homo sapiens] >pir|A34889|XUHUMC methylated-DNA--protein-cysteine S-m	gi|187579	2	694	88	88	HISAV27
370	829302			600	929			HBEJ72
371	829304			300	716			HKAAL43
372	829320	putative [Homo sapiens] >pir|B41648|B41648 protein-tyrosine-phosphatase (EC 3.1.3.48) cdc25B - human >sp|P30305|MPI2_HUMAN M-PHASE INDUCER PHOSPHATASE 2 (EC 3.1.3.48). >gi|2739200 (AF036233) cdc25B phosphatase [Homo sapiens] (SUB 56-338) Length = 566	gi|180173	161	853	100	100	HIBCJ85
373	829322	capping protein alpha subunit isoform 1 [Homo sapiens] >pir|G02639|G02639 capping protein alpha subunit isoform 1 - human >sp|P52907|CAZ1_HUMAN F-ACTIN CAPPING PROTEIN ALPHA-1 SUBUNIT (CAPZ). Length = 286	gi|1336099	3	938	95	95	HJBCY27
374	829355			3	782			HHEAA46

375	829364	initiation factor 2 alpha [Bos taurus] >gi|204002 translational initiation factor eIF-2, alpha subunit [Rattus norvegicus] >pir|A26711|A26711 translation initiation factor eIF-2 alpha chain - rat >pir|S18461|S18461 translation initiation factor eIF-2 alph	gi|325	70	651	88	88	HKAEV74	
376	829919			272	448			HAJAC05	
377	829941	weak similarity to procollagen alpha chain 1(V) chain [Caenorhabditis elegans] >sp|Q20220|Q20220 SIMILARITY TO PROCOLLAGEN ALPHA CHAIN 1(V) CHAIN. Length = 697	gi|1065515	215	796	50	74	HAIBC14	
378	829945			43	222			HAGHF36	
379	829946			2	319			HAHCZ18	
380	829947	(AF033188) WSB-2 [Mus musculus] >sp|O54929|O54929 WSB-2. Length = 404	gi|2766493	1	1206	95	98	HAICN24	
381	829952			478	741			HAICL28	
382	829954	HIV-EP2/Schnurri-2 [Homo sapiens] >gi|187405 MHC binding protein-2 [Homo sapiens] {SUB 1184-1323} Length = 1833	gi|182120	2	853	80	82	HAGDR03	
383	829955	zinc finger protein [Homo sapiens] >sp|Q92951|Q92951 ZINC FINGER PROTEIN. Length = 273	gi|1575615	52	885	99	100	HAGEX65	
384	829957			1	744			HAGEP17	
385	829958	ribosomal protein L22 [Rattus norvegicus] >pir|S52084|S52084 ribosomal protein L22 - rat Length = 128	gi|710295	2	418	62	74	HAECH75	

386	829960	sorbitol dehydrogenase [Homo sapiens] >gi|1755138 sorbitol dehydrogenase [Homo sapiens] >pir|A54674|A54674 L-iditol 2-dehydrogenase (EC 1.1.1.14) - human >sp|G1755138|G1755138 SORBITOL DEHYDROGENASE. Length = 357	gi|520450	2	1069	97	97	HAIBJ62
387	829966	(AF106835) putative DnaJ [Methylovorus sp. strain SS1] >sp|G4008081|G4008081 PUTATIVE DNAJ. Length = 371	gi|4008081	185	505	40	74	HAGAX57
388	829967	histone H1 [Homo sapiens] >pir|S26364|HSHU11 histone H1-1 - human >sp|P16403|H1D_HUMAN HISTONE H1D (H1.2). {SUB 2-213} Length = 213	gi|31968	213	542	81	81	HADDI38
389	829970			3	878			HADBH65
390	829981	transcription factor ATF-3 - human (fragment) Length = 222	pir|C34223|C34223	2	391	70	72	HADFU64
391	829985	nuclear RNA helicase [Homo sapiens] >sp|O00148|O00148 NUCLEAR RNA HELICASE. Length = 427	gi|1905998	26	721	88	88	HACBO61
392	829986	smooth muscle myosin heavy chain isoform SM1 [human, umbilical cord, fetal aorta, Peptide Partial, 330 aa] [Homo sapiens] >pir|I65768|I65768 smooth muscle myosin heavy chain isoform SM1 - human (fragment) >sp|Q16086|Q16086 SMOOTH MUSCLE MYOSIN HEAVY CHAIN	bbs|140615	21	209	100	100	HACBQ88
393	829988			325	849			HACAI04
394	829990			266	454			HADFJ12

395	829991	NGFI-B/nur77 beta-type transcription factor homolog=TINUR [human, T lymphoid cell line, PEER, Peptide, 535 aa] [Homo sapiens] >sp|Q16311|Q16311 TINUR= NGFI-B/NUR77 BETA-TYPE TRANSCRIPTION FACTOR HOMOLOG. Length = 535	bbs|164521	2	286	98	98	HACBV53
396	829992			289	540			HACBX74
397	829993	Not56-like protein [Homo sapiens] >sp|Q92685|NT56_HUMAN NOT56-LIKE PROTEIN. Length = 438	gnl|PID|e276888	3	440	77	77	H6EDW38
398	829998	(AL033385) dna-directed rna polymerase iii subunit [Schizosaccharomyces pombe]	gnl|PID|e1339667	270	830	43	65	H6EDK29
399	829999			14	142			H6BSE17
400	830000	NNP-1 [Homo sapiens] >sp|P56182|NNP1_HUMAN NNP-1 PROTEIN (D21S2056E). Length = 461	gi|2258274	545	856	77	77	H6EEQ39
401	830001	homologous to rat HREV107 (ACC.NO. X76453) [Homo sapiens] Length = 162	gi|1054752	397	903	88	88	H2MBY64
402	830005	alpha 1(XVIII) collagen [Mus musculus] >sp|Q61437|Q61437 PROCOLLAGEN, TYPE XVIII, ALPHA 1 (ALPHA 1 COLLAGEN) (XVIII) (FRAGMENT). Length = 1288	gi|511298	3	347	37	42	H6EEX40
403	830009	TFIIE-beta [Homo sapiens] >bbs|67862 general transcription factor IIE 34 kda subunit, TFIIE 34 kda subunit [human, Peptide, 291 aa] [Homo sapiens] >pir|S29292|S29292 transcription factor TFIIE-beta - human Length = 291	gi|37070	3	1028	93	93	H2LAD85

404	830010	(AF062346) zinc finger protein 216 splice variant 1 [Homo sapiens] >gi|3643811 (AF062347) zinc finger protein 216 splice variant 2 [Homo sapiens] >gi|3668066 (AF062072) zinc finger protein 216 [Homo sapiens] >sp|O76080|O76080 ZINC FINGER PROTEIN 216. >bbs	gi|3643809	1	930	100	100	I12MBU62
405	830127	thymopoietin alpha [Homo sapiens] >pir|A55741|A55741 thymopoietin alpha precursor - human Length = 694	gi|508725	469	1074	77	78	I12MBT25
406	830128			102	770			I12CBI25
407	830129	subunit of coatomer complex [Homo sapiens] >sp|P35606|COPP_HUMAN COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP) (P102). {SUB 2-906} Length = 906	gi|298097	3	2234	100	100	I12CBU57
408	830137	aldehyde dehydrogenase [Homo sapiens] >sp|P30837|DHA5_HUMAN ALDEHYDE DEHYDROGENASE, MITOCHONDRIAL X PRECURSOR (EC 1.2.1.3) (CLASS 2). Length = 517	gi|1263008	2	943	95	95	I12CBX43
409	830140	retroviral proteinase-like protein - human (fragment) Length = 165	pir|JE0065|JE0065	347	784	100	100	I12CBG30
410	830157	(AF043735) 14-3-3 epsilon [Bos taurus] >gi|984319 epsilon 14-3-3 protein [Homo sapiens] >gnl|PID|d1033501 (AB017103) 14-3-3 epsilon [Homo sapiens] >gi|902787 14-3-3 protein epsilon isoform [Homo sapiens] >gi|1184725 14-3-3 protein epsilon isoform [Homo sa	gi|3676399	2	889	99	99	I12CBB64

411	830195	90kDa heat shock protein [Homo sapiens] >pir|A29461|HHHU84 heat shock protein 90-beta - human >sp|P08238|HS9B_HUMAN HEAT SHOCK PROTEIN HSP 90-BETA (HSP 84) (HSP 90). {SUB 2-724} Length = 724	gi|306891	80	631	93	94	HWACG91
412	830196	90kDa heat shock protein [Homo sapiens] >pir|A29461|HHHU84 heat shock protein 90-beta - human >sp|P08238|HS9B_HUMAN HEAT SHOCK PROTEIN HSP 90-BETA (HSP 84) (HSP 90). {SUB 2-724} Length = 724	gi|306891	19	1263	100	100	H2CAC90
413	830409	eIF3-p40 [Homo sapiens] >gi|2351380 translation initiation factor eIF3 p40 subunit [Homo sapiens] >sp|O15372|O15372 EIF3-P40. Length = 352	gi|2351380	325	1092	91	91	HLJDCQ28
414	830417	core protein II precursor [Homo sapiens] >pir|A32629|A32629 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) core protein II - human Length = 453	gi|180928	115	744	81	82	HMCBI54
415	830531	5' half of the product is homologues to Bacillus subtiis SAICAR synthetase, 3' half corresponds to the catalytic subunit of AIR carboxylase [Homo sapiens] >pir|S14147|S14147 multifunctional purine biosynthesis protein - human Length = 425	gi|28384	112	1059	100	100	HMCGQ67
416	830677	pinin [Canis familiaris] >sp|P79149|P79149 PININ. Length = 773	gi|1684845	8	1111	88	88	HLWBS80
417	831355	GTP-binding protein - mouse Length = 198	pir|S39543|S39543	128	730	99	100	HKMAB33
418	831420	(AB016869) p70 ribosomal S6 kinase beta [Homo sapiens] >sp|D1035383|D1035383 P70 RIBOSOMAL S6 KINASE BETA. Length = 495	gnl|PID|d1035383	1	672	91	92	HWBAS06

419	831702	Gem [Homo sapiens] >pir|A54575|A54575 35K GTP-binding protein Gem - human >sp|P55040|GEM_HUMAN GTP-BINDING PROTEIN GEM (GTP-BINDING MITOGEN-INDUCED T-CELL PROTEIN) (RAS-LIKE PROTEIN KIR). Length = 296	gi|544493	100	1107	93	93	H2LAD84	
420	831717	ets2 protein [Homo sapiens] >gi|2736087 (AF017257) erythroblastosis virus oncogene homolog 2 protein [Homo sapiens] >pir|B32066|TVHUE2 transcription factor ets-2 - human >sp|P15036|ETS2_HUMAN C-ETS-2 PROTEIN. >gi|182271 ets protein [Homo sapiens] {SUB 324	gi|182273	278	1309	90	90	HLLBB45	
421	832488	tissue-specific secretory protein [unidentified] >gi|320511 HE4 protein [Homo sapiens] >pir|S25454|S25454 HE4 protein - human >sp|Q14508|EP4_HUMAN MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR (HE4) (EPIDIDYMAL SECRETORY PROTEIN E4). Length = 125	gi|583141	24	434	98	100	HKMLZ60	48
422	833207	secretory granule proteoglycan peptide core [Homo sapiens] >gi|338062 protcoglycan secretory granule 1 [Homo sapiens] >gi|32433 hematopoetic proteoglycan core protein (AA 1 - 158) [Homo sapiens] >pir|A35183|A28058 secretory granule proteoglycan core prote	gi|190420	57	542	81	81	HWAFH33	
423	835940	putative Rab5-interacting protein {clone L1-57} [human, HeLa cells, Peptide Partial, 122 aa] [Homo sapiens]	bbs|180090	126	464	78	81	HNFHV44	
424	836953	GTP-binding protein [Homo sapiens] >pir|G34323|G34323 GTP-binding protein Rab6 - human	gi|550072	388	1038	99	99	HMEFS23	

425	837105			860	1168			HL1AS90
426	837300			276	494			HODHJ94
427	837373	ribosomal protein L5 [Homo sapiens] >pir|S55912|S55912 ribosomal protein L5, cytosolic - human >gi|1658578 ribosomal L5 protein [Homo sapiens] {SUB 153-297} Length = 297	gi|550013	1	714	98	98	HIASC92
428	837687	protein trafficking protein [Homo sapiens] >gnl|PID|e239969 transmembrane protein [Homo sapiens] >gnl|PID|e1309760 (AJ004913) integral membrane protein, Tmp21-I (p23) [Homo sapiens] >pir|G01159|G01159 protein trafficking protein tmp21-I - human >sp|E13097	gi|1407826	435	953	98	98	HSLBF05
429	837991			1	294			HPJCY94
430	838442	procollagen C-proteinase [Homo sapiens] >sp|Q13292|Q13292 PROCOLLAGEN C-PROTEINASE. Length = 986	gi|1245357	3	506	97	97	HAUBJ52
431	840541	cyclin C [Homo sapiens] >pir|A40268|A40268 cyclin C - human >sp|P24863|CG1C_HUMAN G1/S-SPECIFIC CYCLIN C. Length = 303	gi|1117984	127	549	99	100	HWHQA57
432	840543	(AF016369) U4/U6 small nuclear ribonucleoprotein hPrp4 [Homo sapiens] >sp|O43445|O43445 U4/U6 SMALL NUCLEAR RIBONUCLEOPROTEIN HPRP4. Length = 522	gi|2708305	40	1020	94	94	HWBEJ29
433	840550			1	141			HWBFM54
434	840563			382	723			HADFY02
435	840565	AZ-1 [Mus musculus] >gnl|PID|d1008454 pre-acrosome localization protein [Mus musculus] >pir|S63993|S63993 acrosomal protein AZ1 - mouse >sp|Q62036|Q62036 5-AZACYTIDINE INDUCED PROTEIN (PRE-ACROSOME LOCALIZATION PROTEIN). Length = 1060	gnl|PID|d1019745	1	300	71	88	HHGCW14

436	840569			2	136			HPRBG41
437	840570	p116Rip [Mus musculus] >sp|P97434|P97434 P116RIP. Length = 1024	gi|1657837	2	691	90	91	HOEDH35
438	840571			873	1097			HIBCA19
439	840573	S-adenosyl homocysteine hydrolase homolog [Homo sapiens] Length = 500	gi|2852125	3	719	74	74	HYAAB09
440	840574			2	292			HWLBN43
441	840575	KERATIN, TYPE I CYTOSKELETAL 10 (CYTOKERATIN 10) (K10) (CK 10). >sp|G244509|G244509 KERATIN 10 V2 SUBDOMAIN 142 AMINO ACID VARIANT. {SUB 452-593} Length = 593	sp|P13645|K1CJ_HUMAN	3	1856	100	100	HWEAD52
442	840579			50	1549			HAPBL12
443	840580			343	867			HWLFE67
444	840581			21	191			HYAAY95
445	840605	(AJ000480) phosphoprotein [Homo sapiens] >sp|O15180|O15180 PHOSPHOPROTEIN (FRAGMENT). Length = 224	gnl|PID|e329709	3	170	97	97	HWTAI85
446	840607	alpha-adaptin (A) (AA 1-977) [Mus musculus] >pir|A30111|A30111 alpha-adaptin A - mouse >sp|P17426|ADAA_MOUSE ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPT	gi|49878	3	317	98	98	HTYSE72
447	840609	olfactomedin [Rana catesbeiana] >pir|A47442|A47442 olfactomedin precursor - bullfrog >sp|Q07081|OLFM_RANCA OLFACTOMEDIN PRECURSOR (OLFACTORY MUCUS PROTEIN). Length = 464	gi|294502	1	201	46	75	HUFBD83

448	840610	plakoglobin [Homo sapiens] >sp|Q15151|Q15151 PLAKOGLOBIN. >gnl|PID|d1010077 plakoglobin [Homo sapiens] {SUB 239-409} Length = 745	gnl|PID|e214034	1784	2818	94	94	HBGNU40
449	840611			657	848			HUFAT62
450	840612	B-IND1 protein [Mus musculus] >sp|O09003|O09003 B-IND1 PROTEIN. Length = 189	gnl|PID|e1192419	130	1242	85	86	HWLFV07
451	840615	casein kinase II alpha subunit [Bos taurus] >gi|611 casein kinase alpha subunit [Bos taurus] >gi|177994 casein kinase II alpha subunit [Homo sapiens] >gi|598147 casein kinase II alpha subunit [Homo sapiens] >pir|A30319|A30319 casein kinase II (EC 2.7.1.-)	gi|162777	140	1234	94	94	HUKDT16
452	840622			135	962			HTXNQ26
453	840623	1,4-alpha-glucan branching enzyme [Homo sapiens] >pir|A46075|A46075 glycogen branching enzyme - human >sp|Q04446|GLGB_HUMAN 1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYCOGEN BRANCHING ENZYME) (BRANCHER ENZYME). Length = 702	gi|184026	3	542	97	98	HTTEK41
454	840624			1065	1550			HTXBO36

455	840631	(AL033514) predicted using Genefinder; cDNA EST yk465c10.5 comes from this gene [Caenorhabditis elegans] >sp|E1358418|E135841 8 Y75B8A.16 PROTEIN. Length = 431	gnl|PID|e1358418	3	1250	53	73	HTTDU70

456	840632			1241	1453			HTTFY74
457	840633			1	612			HTTFA16
458	840634			232	438			HTTFG83
459	840635			35	748			HTXBW79
460	840636			134	382			HTWIH73
461	840637			315	551			HTTEZ16
462	840639			1035	1700			HTTET75
463	840640	(AC004684) putative ribotol dehydrogenase [Arabidopsis thaliana] >sp|O80924|O80924 PUTATIVE RIBOTOL DEHYDROGENASE. Length = 321	gi|3236237	2	418	31	50	HTQDA44
464	840650			86	940			HTPAG74
465	840652	spermatid perinuclear RNA binding protein [Mus musculus] >pir|A57284|A57284 spermatid perinuclear RNA-binding protein Spnr - mouse >sp|Q62262|Q62262 SPERMATID PERINUCLEAR RNA-BINDING PROTEIN.	gi|673454	1	588	89	89	HTTCB17

Length = 648

466	840653			3	989			HTTDG56
467	840655			1	2139			HTPCP50
468	840659	(AF016507) C-terminal binding protein 2 [Homo sapiens] >sp|P56545|CTB2_HUMAN C-TERMINAL BINDING PROTEIN 2. Length = 445	gi|2909777	511	1518	89	89	HTSHH54
469	840660			293	520			HTQJF77
470	840661			3	710			HTLGP71
471	840662	cleavage signal 1 protein [Homo sapiens] >pir|JH0629|JH0629 cleavage signal-1 protein - human >sp|P28290|CS1_HUMAN CLEAVAGE SIGNAL-1 PROTEIN (CS-1). Length = 249	gi|181123	494	1333	90	92	HTOEY44
472	840663			179	466			HTPBY35
473	840670			1132	1647			HTTBJ61
474	840671			210	1001			HTJMJ95
475	840672	(AF037448) Gry-rbp [Homo sapiens] >sp|O60506|O60506 GRY-RBP. Length = 623	gi|3037013	3	1739	99	99	HTHDF09
476	840673	complement component C1s [Homo sapiens] >gi|179648 complement subcomponent C1s precursor [Homo sapiens] >gi|763110 complement protein C1s precursor [Homo sapiens] >pir|A40496|C1HUS complement subcomponent C1s (EC 3.4.21.42) precursor - human >sp|P09871|C1	gi|179646	1	690	98	98	HTJAA66
477	840674	glypican [Homo sapiens] >pir|A36347|A36347 glypican 1 precursor - human >sp|P35052|GLYP_HUMAN GLYPICAN-1	gi|31847	208	525	87	87	HTLDZ68

PRECURSOR. Length = 558

478	840677			237	1010			HTJNE24
479	840678			3	842			HTGFX11
480	840680	Similarity to H.influenza ribonuclease PH (SW:RNPH_HAEIN);	gnl|PID|e1343517	115	555	48	72	HTLEI30
481	840691	polynucleotide adenylyltransferase [Bos taurus] >sp|P25500|PAP_BOVIN POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE). {SUB 2-739} Length = 739	gi|605	1	900	68	70	HTEKG75
482	840700			54	998			HTELT78
483	840701			879	1370			HDQDW52
484	840702			713	955			HTEJY89
485	840705			106	621			HTELU22
486	840715	stanniocalcin [Homo sapiens] >gi|975298 stanniocalcin precursor [Homo sapiens] >sp|P52823|CSTP_HUMAN STANNIOCALCIN PRECURSOR.	gi|1199620	1	828	99	99	HSYBK03
487	840717			561	1058			HSSNA42
488	840718	(AC005154) similar to protein U28928 (PID:g861306) [Homo sapiens] >sp|O75223|O75223 WUGSC:H_DJ0777O23.1 PROTEIN. Length = 188	gi|3242764	227	562	98	98	HSSMV32
489	840719			3	284			HSSNB31
490	840724	metallothionein I-F [Homo sapiens] >gi|386866 human metallothionein-IF [Homo sapiens] >pir|B22634|SMHU1F metallothionein 1F - human >sp|P04733|MT1F_HUMAN	gi|386867	226	510	100	100	HSVBQ73

		METALLOTHIONEIN-IF (MT-1F). Length = 61						
491	840725	Unknown		1259	1501			HSRDA46
492	840727			4	606			HSXCO55
493	840731	apg-2 [Mus musculus] >sp|Q61316|HS74_MOUSE HEAT SHOCK 70-RELATED PROTEIN APG-2. Length = 841	gnl|PID|d1013599	22	471	69	75	HSSAO67
494	840733			3	437			HSSGG96
495	840734			228	365			HSRFE65
496	840736	small nuclear ribonucleic protein [Homo sapiens] Length = 92	gi|338259	58	342	100	100	HSRFE95
497	840737			3	341			HSSFS95
498	840739			196	561			HSLJW05
499	840746	similar to mouse CC1. [Homo sapiens] >sp|Q92601|Q92601 MYELOBLAST KIAA0202. Length = 1591	gnl|PID|d1013883	452	1420	85	85	HSLII31
500	840748	cytoplasmic antiproteinase, CAP=38 kda intracellular serine proteinase inhibitor [human, placenta, Peptide, 376 aa] [Homo sapiens] Length = 376	bbs|145232	65	1441	96	96	HSRGX11
501	840750	(AC002339) putative ABC transporter [Arabidopsis thaliana] >sp|O22950|O22950 ABC TRANSPORTER ISOLOG, 3' PARTIAL (FRAGMENT). Length = 664	gi|2335109	507	845	34	62	HSODA53
502	840751	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN]. Length = 1913	sp|Q15746|KMLS_HUMAN	3	2519	90	90	HTEFV12

503	840757	(AB005624) rig-analog DNA-binding protein [Sus scrofa] >gi|306898 rig-analog protein (putative); putative [Homo sapiens] >gi|337416 human homologue of rat insulinoma gene (rig); putative [Homo sapiens]	gnl|PID|d1022359	236	568	100	100	HKBAL84
504	840759	transcription factor ZFM1 [Homo sapiens] >sp|Q15913|Q15913 TRANSCRIPTION FACTOR ZFM1. Length = 571	gi|1100209	481	2073	100	100	HSLDB56
505	840760			233	529			HSKDG51
506	840770	FORMATE ACETYLTRANSFERASE 2 (EC 2.3.1.54) (PYRUVATE FORMATE-LYASE 2) (FRAGMENT). Length = 716	sp|D1036490|D1036490	1	195	100	100	HSLCS52
507	840781	glyoxalase I [Homo sapiens] >gnl|PID|d1003075 lactoyl glutathione lyase [Homo sapiens] >pir|A46714|A46714 lactoylglutathione lyase (EC 4.4.1.5) - human	gi|183258	107	673	99	99	HSKHK35
508	840789	(AC003003) Homolog of rat B/K protein product [Homo sapiens] >sp|O43330|O43330 HUMAN HOMOLOGUE OF RAT B/K PROTEIN PRODUCT (FRAGMENT). Length = 361	gi|2865208	1	657	93	93	HHPSF20
509	840790			216	347			HHKSC89
510	840791			2	817			HHSGD58
511	840798	polynucleotide phosphorylase (PNPase) [Bacillus subtilis] >gi|1184680 polynucleotide phosphorylase [Bacillus subtilis] >pir|S70691|S70691 polyribonucleotide nucleotidyltransferase (EC 2.7.7.8) alpha chain pnpA - Bacillus subtilis >sp|P50849|PNPA_BACSU POL	gnl|PID|e1185260	2	493	41	66	HHERQ85
512	840802	(AB001915) NG,NG-dimethylarginine dimethylaminohydrolase [Homo sapiens] Length = 285	gnl|PID|d1038106	1	618	97	98	HHFES15

513	840803	zinc finger protein [Molgula oculata] >sp|Q25473|Q25473 ZINC FINGER PROTEIN. Length = 558	gi|308967	1	1935	36	63	HHERC56
514	840809			2	208			HHEPE84
515	840811			1	690			HHFBP51
516	840813			2	214			HHEMJ45
517	840814	(AL022162) dJ454M7.1.1 (Lowe Oculocerebrorenal Syndrome protein OCRL-1) (isoform 1) [Homo sapiens] >gnl|PID|e244699 Lowe oculocerebrorenal syndrome (OCRL) [Homo sapiens] {SUB 336-813} Length = 813	gnl|PID|e1371023	2	154	100	100	HGBIC73
518	840817	(AB004903) STAT induced STAT inhibitor-2 [Homo sapiens] >gi|3265033 (AF037989) STAT-induced STAT inhibitor-2 [Homo sapiens] >sp|O14508|O14508 STAT INDUCED STAT INHIBITOR-2. Length = 198	dbj|AB004903_1	85	864	99	99	HHEBI06
519	840825			2	436			HHEAB14
520	840826			2022	2360			HHBFD61
521	840827			14	817			HHEAH66
522	840828	Cleavage and Polyadenylation Specifity Factor protein [Bos taurus] >sp|P79101|P79101 CLEAVAGE AND POLYADENYLATION SPECIFITY FACTOR PROTEIN. Length = 684	gnl|PID|e225428	2	1180	98	99	HHEAK56
523	840829			130	618			HFVIE96
524	840831			1166	1447			HFXCN75
525	840836			18	566			HFXKK43
526	840837	(AC005757) R32611_2 [Homo sapiens] >sp|O75865|O75865 R32611_2 (FRAGMENT). Length = 160	gi|3688090	322	759	62	80	HGBAG76
527	840838	(AF006386) axonemal dynein light chain [Homo sapiens] >sp|O14645|O14645 AXONEMAL DYNEIN LIGHT CHAIN. Length = 257	gi|2352534	2	832	100	100	HFXJP72

528	840841			2	790			HGAMD29
529	840842			216	791			HFPCK56
530	840843			12	791			HFVGM54
531	840845			669	1031			HGBBY80
532	840847			151	1044			HFPCN94
533	840851			470	2047			HFOXS46
534	840853			15	224			HFOXV75
535	840854			149	1183			HFPBK03
536	840858	(AC002333) molybdenum cofactor biosynthesis protein E isolog [Arabidopsis thaliana] >sp|O22827|O22827 MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN E ISOLOG. Length = 198	gi|2281094	249	833	41	51	HFPCP42
537	840859	Gu protein [Homo sapiens] >pir|PC6010|PC6010 RNA helicase Gu - human (fragment) >sp|Q13436|Q13436 NUCLEOLAR RNA HELICASE GU (FRAGMENT). Length = 801	gi|1230564	3	1163	63	74	HFOYQ50
538	840863			1	165			HFHW33
539	840868	argininosuccinate lyase [Homo sapiens] >gi|179091 argininosuccinate lyase [Homo sapiens] >pir|A31658|WZHURS argininosuccinate lyase (EC 4.3.2.1) - human Length = 464	gi|179089	2	1678	99	99	HFKEN53
540	840869	(AF064244) intersectin long form [Homo sapiens] >sp|G3859855|G3859855 INTERSECTIN LONG FORM. >gi|3859853 (AF064243) intersectin short form [Homo sapiens] {SUB 1-1220} >gi|3930533 (AF064247) intersectin long form [Homo sapiens] {SUB 1209-1263} Length = 172	gi|3859855	33	632	74	88	HFKFG36
541	840870			505	831			HFKFN13
542	840875			3	617			HFITH86

543	840876	(AC004392) Contains similarity to gb|U51898 Ca2+-independent phospholipase A2 from Rattus norvegicus. [Arabidopsis thaliana] >sp|O80693|O80693 F8K4.6 PROTEIN. Length = 1265	gi|3367519	1	1110	45	70	HFIZQ25
544	840881	histone H2B.1 [Homo sapiens] >gnl|PID|e1301465 (AJ223353) Histone H2B [Homo sapiens] >gi|51306 histone H2B-291B (AA 1 - 126) [Mus musculus] >pir|S04153|S04153 histone H2B (clone 291B) - mouse >pir|F40335|F40335 histone H2B.1 (b) - human >sp|E1301465|E1301	gi|184080	3	449	77	77	HFIIR54
545	840883			3	428			HFIIA80
546	840886	(AJ000506) Homeodomain protein Meis2c [Mus musculus] >sp|P97367|MEI2_MOUSE HOMEOBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1). Length = 477	gnl|PID|e330082	71	964	90	90	HHPDW66
547	840887			1202	1600			HFIIR82
548	840891	RNA polymerase I subunit A12.2 [Saccharomyces cerevisiae] >gi|1019685 ORF YJR063w [Saccharomyces cerevisiae] >gi|531231 RNA polymerase I A12.2 subunit [Saccharomyces cerevisiae] >gi|1015737 ORF YJR063w [Saccharomyces cerevisiae] >pir|A48107|A48107 DNA-dir	gi|172462	250	375	64	86	HFCBQ77
549	840892	histone H2B [Homo sapiens] >pir|I37445|I37445 histone H2B.1 - human >sp|P33778|H2B0_HUMAN HISTONE H2B.1. {SUB 2-126} Length = 126	gi|31977	3	410	98	98	HFEBK16

550	840894	(AF002697) E1B 19K/Bcl-2-binding protein Nip3 [Homo sapiens] >sp|O14620|O14620 E1B 19K/BCL-2-BINDING PROTEIN NIP3. Length = 194	gi|2511529	1	705	80	80	HFHIO60	
551	840896	Cdc73p [Saccharomyces cerevisiae] >pir|S59383|S59383 probable membrane protein YLR418c - yeast (Saccharomyces cerevisiae) >sp|Q06697|Q06697 CHROMOSOME XII COSMID 9931. Length = 393	gi|632679	425	1249	28	57	HFIAL02	
552	840897	syntaxin-4 [Homo sapiens] >gnl|PID|e332032 (AJ000541) syntaxin 4 precursor [Homo sapiens] >gi|2570870 (AF026007) syntaxin 4 [Homo sapiens] >pir|S52726|S52726 syntaxin-4 - human Length = 297	gi|758105	3	1142	100	100	HFIAW49	
553	840898			2	265			HFEBI76	60
554	840904			396	1802			HFITW62	
555	840905	DNA fragmentation factor-45 [Homo sapiens] >sp|O00273|DF45_HUMAN DNA FRAGMENTATION FACTOR-45 (DFF-45). Length = 331	gi|2065561	3	1100	95	95	HETBS69	
556	840908	KIAA0156 gene product is related to Xenopus nucleolin. [Homo sapiens] >sp|Q15020|Q15020 ORF. Length = 963	gnl|PID|d1010577	348	2081	87	87	HETCI63	
557	840909	3-methyl-adenine DNA glycosylase [Homo sapiens] Length = 298	gnl|PID|e224269	2	949	94	94	HEQAN83	
558	840910			103	348			HFKHD68	
559	840912			1530	1754			HFIPBB92	
560	840916	MAL protein [Homo sapiens] >gi|435478 MAL-a gene product [Homo sapiens] >gnl|PID|e1192240 MAL. [Homo sapiens] >pir|A29472|A29472 T-cell surface glycoprotein MAL, splice form a - human	gi|307157	1	432	86	93	HETJW92	

561	840917			518	886			HETIZ12
562	840918	(AF020038) NADP-dependent isocitrate dehydrogenase [Homo sapiens] >gi|3641398 (AF020038) NADP-dependent isocitrate dehydrogenase [Homo sapien	gi|3641398	231	1508	99	99	HAJCO38
563	840922			839	1033			HELGB82
564	840923			1044	1289			HEQAN39
565	840927			119	364			HEMFU44
566	840928			2	1258			HEMCG01
567	840929	helix-loop-helix phosphoprotein [Homo sapiens] >gi|292055 helix-loop-helix phosphoprotein [Homo sapiens] >pir|I53020|I53020 G-0/G-1 switch regulatory protein 8 - human >pir|I65984|I65984 helix-loop-helix phosphoprotein - human Length = 211	gi|292037	3	662	92	92	HEOMQ95
568	840930	(AF002282) alpha-actinin-2 associated LIM protein [Homo sapiens] >sp|O60440|O60440 ALPHA-ACTININ-2 ASSOCIATED LIM PROTEIN. Length = 316	gi|3138924	3	1019	99	99	HEGAD28
569	840931	similar to thiolesterase;	gnl|PID|e1343797	1	1164	49	67	HEMEC70
570	840941			2	781			HEGAL15
571	840944	cofactor E [Homo sapiens] >sp|Q15813|Q15813 COFACTOR E. Length = 527	gi|1465772	822	1685	98	98	HELFC44
572	840945			1067	1435			HEEAS77
573	840948	lanosterol synthase [human, fetal liver, Peptide, 732 aa] [Homo sapiens] >gnl|PID|d1010523 lanosterol synthase [Homo sapiens] >gi|951314 2,3-oxidosqualene-lanosterol cyclase [Homo sapiens] >pir|JC4194|JC4194 lanosterol synthase (EC 5.4.99.7) - human >sp|P	bbs|176180	3	326	99	100	HE9ST22

574	840949	(AJ005324) glutamate permease [synthetic construct] >gnl|PID|e1360147 (AJ005327) glutamate permease [synthetic construct] >gnl|PID|e1360153 (AJ005330) glutamate permease [synthetic construct] Length = 459	gnl|PID|e1360141	3	101	95	95	HE9RM92
575	840953	P43=mitochondrial elongation factor homolog [human, liver, Peptide, 452 aa] [Homo sapiens] >pir|I53499|I53499 translation elongation factor TU-like protein P43, mitochondrial - human Length = 452	bbs|160014	1	1437	100	100	HELGM94
576	840954	RNase L inhibitor (clone 8) - human Length = 599	pir|S63672|S63672	69	1949	95	95	HE9HC20
577	840958	FUSE binding protein 2 [Homo sapiens] >sp|Q92945|Q92945 FUSE BINDING PROTEIN 2 (FRAGMENT). Length = 652	gi|1575607	154	465	57	58	HFLVB33
578	840960	phosphomannose isomerase [Homo sapiens] >pir|S41122|S41122 mannose-6-phosphate isomerase (EC 5.3.1.8) - human >sp|P34949|MANA_HUMAN MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) (PHOSPHOMANNOSE ISOMERASE) (PMI) (PHOSPHOHEXOMUTASE). {SUB 2-423} Length = 423	gi|416017	224	670	100	100	HEEAD70
579	840968			375	2222			HEBFH29
580	840969			1054	1530			HE9PB53
581	840972			1	387			HE8UU14
582	840973			548	874			HE9DI68
583	840975			1	159			HE9GO90
584	840978			1433	1765			HE9NG78

585	840980	nerve growth factor [Homo sapiens] >gi|32031 pleiotrophin [Homo sapiens] >bbs|119887 pleiotrophin, PTN [human, Peptide, 168 aa] [Homo sapiens] >bbs|130735 heparin-binding neurite outgrowth promoting factor, HBNF {alternatively spliced} [human, Peptide, 16	gi|183890	75	833	90	90	HE8FE14
586	840982			81	359			HE8ES49
587	840985			3	830			HE8UK50
588	840989	(AB016247) sterol-C5-desaturase [Homo sapiens] >sp|O75845|O75845 STEROL-C5-DESATURASE (EC 1.3.3.2) (LATHOSTEROL OXIDASE). Length = 299	gnl|PID|d1034698	107	1027	99	100	HE8FM74
589	840991	(AF032886) forkhead protein [Homo sapiens] >sp|O43524|O43524 FORKHEAD PROTEIN. Length = 673	gi|2895494	861	1559	81	81	HE8FA09
590	840996	ATP:citrate lyase [Homo sapiens] >sp|Q13037|Q13037 ATP:CITRATE LYASE. Length = 1101	gi|603074	818	1906	99	99	HE8MY23
591	840997	LIV-1 protein [Homo sapiens] >pir|G02273|G02273 LIV-1 protein - human >sp|Q13433|Q13433 ESTROGEN REGULATED LIV-1 PROTEIN. Length = 752	gi|1256001	3	1193	75	75	HE8DR57
592	840998			1	390			HE2BN26
593	840999			855	1013			HE8DJ30
594	841000			1	279			HE6DC57
595	841002			363	812			HE8BT63
596	841003			94	315			HE2DX28
597	841008	Aop1_Human, MER5(Aop1_Mouse)-like protein [Homo sapiens] >gi|854126 humer [Homo sapiens] {SUB 227-256} Length = 256	gnl|PID|d1008985	1	672	99	99	HE8AU49

598	841013	(AB011004) UDP-N-acetylglucosamine pyrophosphorylase [Homo sapiens] >sp|Q16222|Q16222 AGX-1 ANTIGEN (FRAGMENT). Length = 505	gnl|PID|d1032151	265	1836	99	99	HDTAU64	
599	841014	fumarase precursor [Homo sapiens] >gi|4097195 fumarase [Homo sapiens] >sp|P07954|FUMH_HUMAN FUMARATE HYDRATASE, MITOCHONDRIAL PRECURSOR (EC 4.2.1.2) (FUMARASE). >sp|G4097195|G4097195 FUMARASE (EC 4.2.1.2). Length = 510	gi|1545996	178	1185	96	96	HE2EB32	
600	841015			48	425			HE2DT31	
601	841018			1	150			HE2EA79	
602	841019			94	228			HDTGC76	
603	841024	Ran [Canis familiaris] >gi|190879 ras-like protein [Homo sapiens] >gi|2967848 (AF052578) androgen receptor associated protein 24 [Homo sapiens] >gi|727167 Ran [Mus musculus] >bbs|180269 GTP-binding protein [mice, C3H/HeJ spleens, LDS responder, Peptide, 2	gi|924	34	750	100	100	HE9CO25	64
604	841025			75	401			HDTDZ04	
605	841026			3	599			HDTGP42	
606	841027			1	489			HDRMB48	
607	841029	Id-2H [Homo sapiens] >pir|A40227|A40227 transcription repressor Id-2 - human >sp|Q02363|ID2_HUMAN DNA-BINDING PROTEIN INHIBITOR ID-2. Length = 134	gnl|PID|d1003496	1	528	100	100	HDTAG94	
608	841030			515	721			HDTGK45	
609	841031			23	145			HDSAL27	

610	841034	G-rich sequence factor-1 [Homo sapiens] >gi|517196 G-rich sequence factor-1 [Homo sapiens] >sp|Q12849|GRF1_HUMAN G-RICH SEQUENCE FACTOR-1 (GRSF-1). >pir|S48081|S48081 GRSF-1 protein - human (fragment) {SUB 94-424} Length = 424	gi|517196	267	449	95	98	HDQDH60
611	841036			1201	1542			HDPTM31
612	841039	(AC002340) putative RNA helicase A, 5' partial [Arabidopsis thaliana] >sp|O49345|O49345 PUTATIVE RNA HELICASE A, 5' PARTIAL (FRAGMENT). Length = 1114	gi|2880057	763	2112	60	76	HDQFB71
613	841040	(AF071202) ABC transporter MOAT-B [Homo sapiens] >sp|G3335173|G3335173 ABC TRANSPORTER MOAT-B. Length = 1325	gi|3335173	2	1339	92	92	HDQDF77
614	841048			1	1338			HDPXU60
615	841049	(AC003682) ZNF134 [Homo sapiens] >sp|G2689444|G2689444 ZNF134. Length = 427	gi|2689444	3	347	97	97	HDPXK77
616	841050			705	947			HDPUP64
617	841052	monoamine oxidase A [Homo sapiens] >gi|187353 monoamine oxidase A [Homo sapiens] >gi|187355 monoamine oxidase A [Homo sapiens] >pir|A36175|A36175 amine oxidase (flavin-containing) (EC 1.4.3.4) A - human >sp|P21397|AOFA_HUMAN AMINE OXIDASE [FLAVIN-CONTAINI	gi|187351	1	1194	95	95	HDPRJ46
618	841054			60	1262			HDPXL80
619	841055			23	346			HDPMK92
620	841056			492	695			HDPVB33
621	841060			612	851			HDPXB24

622	841061	quinone oxidoreductase [Homo sapiens] >gi|516534 quinone oxidoreductase2 [Homo sapiens] >pir|A32667|A32667 NAD(P)H dehydrogenase (quinone) (EC 1.6.99.2) 2 - human Length = 231	gi|190818	21	614	100	100	HPIBQ60
623	841062	histone deacetylase HDI [Homo sapiens] >sp|Q13547|HDA1_HUMAN HISTONE DEACETYLASE 1 (HD1). Length = 482	gi|1277084	67	1530	90	90	HDPPA96
624	841063	(AI.009194) SWISS-PROT:P38861; NONSENSE-MEDIATED MRNA DECAY PROTEIN 3.; SACCHAROMYCES CEREVISIAE	gnl|PID|e1251068	2	592	69	82	HDPJQ57
625	841067	mannosyl-oligosaccharide 1,2-alpha-mannosidase (EC 3.2.1.113) - rabbit (fragment) >gi|474282 mannosyl-oligosaccharide alpha-1,2-mannosidase [Oryctolagus cuniculus] {SUB 12-480} Length = 480	pir|B54408|B54408	2	592	59	83	HDPQE64
626	841074	14.3.3 protein [Homo sapiens] >gi|32464 HS1 gene product [Homo sapiens] >pir|S15076|S15076 protein kinase regulator 14.3.3 - human >sp|P27348|143T_HUMAN 14-3-3 PROTEIN TAU (14-3-3 PROTEIN THETA) (14-3-3 PROTEIN T-CELL) (HS1 PROTEIN). >gi|3387922 (AF070556	gi|23222	188	907	98	99	HE8NS76
627	841076			96	755			HDPMG95
628	841081	(AE000715) ribosomal protein L20 [Aquifex aeolicus] >pir|C70382|C70382 ribosomal protein L20 - Aquifex aeolicus >sp|O67086|O67086 50S RIBOSOMAL PROTEIN L20. Length = 118	gi|2983472	2	541	41	65	HDPQC09
629	841083			1	480			HDPCX80
630	841089			321	551			HDPND16

631	841093	(AF035646) Rab10 [Mus musculus] >sp|O88386|O88386 RAB10. Length = 200	gi|3406428	479	1132	100	100	HDPPI29
632	841097	(AF090867) guanosine monophosphate reductase [Rattus norvegicus] >sp|G3907579|G3907579 GUANOSINE MONOPHOSPHATE REDUCTASE. Length = 345	gi|3907579	267	1061	78	90	HDPEB78
633	841098	GATA-binding protein [Homo sapiens] >pir|A40815|A40815 transcription factor GATA-2 (version 1) - human >sp|P23769|GAT2_HUMAN ENDOTHELIAL TRANSCRIPTION FACTOR GATA-2. Length = 480	gi|182996	1	384	90	91	HDABX64
634	841101	phosphatidylcholine transfer protein [Bos taurus] >pir|A91092|EPBO phosphatidylcholine transfer protein - bovine >sp|P02720|PPCT_BOVIN PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP). Length = 213	gi|710419	3	1004	35	55	HDPBQ32
635	841113	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (hpcE) [Methanococcus jannaschii] >pir|F64506|F64506 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase homolog - Methanococcus jannaschii >sp|Q59050|Q59050 HYPOTHETICAL PROTEIN MJ1656. Length = 237	gi|1500558	133	1137	50	74	HDBAE85
636	841115			58	396			HDLAZ62
637	841116			47	682			HDPBJ61
638	841117			1	1179			HDFMB93
639	841125			1	117			HCYBI78
640	841127			2	859			HDABQ85

641	841128	collagenase stimulatory factor [Homo sapiens] >gi|1209374 amino acid feature: intracellular domain, aa 707 .. 829; amino acid feature: transmembrane domain, aa 638 .. 706; amino acid feature: extracellular domain, aa 86 .. 637 [Homo sapiens] >gi|34449 M6	gi|409357	64	891	100	100	HDPFH18	
642	841132			1	1428			HDPFI70	
643	841133	myosin-I, Myr 1c (alternatively spliced) - rat Length = 1078	pir|B45439|B45439	4	1710	89	91	HCYBL17	
644	841134	gamma SNAP [Homo sapiens] Length = 312	gi|1685288	2	802	100	100	HDAAC32	
645	841135	homologous to mouse gene PC326:GenBank Accession Number M95564 [Homo sapiens] >sp|Q12839|Q12839 (H326). Length = 597	gi|458692	124	765	81	81	HDABE30	
646	841136			514	735			HCQDF95	
647	841138	imogen 38 [Homo sapiens] >sp|Q92665|Q92665 IMOGEN 38. Length = 395	gnl|PID|e218584	3	1238	80	80	HDABK25	
648	841139			347	478			HCQBH60	
649	841141			192	833			HDPBQ85	
650	841142			452	1051			HCQAM05	
651	841145			1022	1366			HCNSQ35	
652	841146			864	1061			HCMSW06	
653	841150	(AF038957) translation initiation factor 4e [Homo sapiens] >sp|O75349|O75349 TRANSLATION INITIATION FACTOR 4E. Length = 236	gi|3329384	115	387	83	86	HCQAG10	

654	841153	argininosuccinate synthetase [Homo sapiens] >gi|28872 argininosuccinate synthetase (aa 1-412) [Homo sapiens] >pir|A01195|AJHURS argininosuccinate synthase (EC 6.3.4.5) - human >sp|P00966|ASSY_HUMAN ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPA	gi|179057	1207	2532	96	96	HCYBC10	
655	841154	(AF084260) signalosome subunit 2 [Homo sapiens] >gi|3639069 (AF087688) alien-like protein [Mus musculus] >sp|O88950|O88950 ALIEN-LIKE PROTEIN. >sp|G3514097|G3514097 SIGNALOSOME SUBUNIT 2. >gi|3309166 (AF071312) COP9 complex subunit 2 [Mus musculus] {SUB 4	gi|3514097	1	1368	100	100	HCMSB29	
656	841156	carcinoma-associated antigen GA733-2 [Homo sapiens] >gi|182906 carcinoma-associated antigen GA733-2 [Homo sapiens] >pir|B48149|B48149 epithelial glycoprotein antigen GA733-2 precursor - human Length = 314	gi|182896	6	1130	86	86	HCIAA60	69
657	841157	collagen pro-alpha-1 type I chain [Mus musculus] >pir|S57243|S21626 collagcn alpha 1(I) chain precursor - mouse >sp|P11087|CA11_MOUSE PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR. >gi|192262 pro-alpha-1 type I collagen [Mus musculus] {SUB 518-1128} >gi|192264 p	gi|470674	88	336	36	42	HCHCJ07	
658	841159			510	818			HCLCK84	
659	841164			2	463			HCHAZ66	
660	841167			982	1305			HCHOG20	

661	841170	SRp30c [Homo sapiens] >gnl|PID|e1248292 (AL021546) pre-mRNA splicing factor SRp30c [Homo sapiens] >gi|4099429 splicing factor SRp30c [Homo sapiens] >pir|S59075|S59075 splicing factor SRp30c - human >sp|G4099429|G4099429 SPLICING FACTOR SRP30C. Length = 22	gi|1049078	2	760	81	81	HCHOE21
662	841173	spermidine synthase [Homo sapiens] >pir|A32610|A32610 spermidine synthase (EC 2.5.1.16) - human Length = 302	gi|338394	2	931	97	97	HCHBQ07
663	841176			561	683			HCFOI36
664	841178	thyroid receptor interactor [Homo sapiens] Length = 152	gi|703110	65	460	99	100	HCGBQ34
665	841180	(AF029777) hGCN5 [Homo sapiens] >sp|G3220164|G3220164 HGCN5. >gi|1491935 histone acetyltransferase [Homo sapiens] {SUB 362-837} >sp|G1911495|G1911495 HGCN5=TRANSCRIPTIONAL ADAPTOR. {SUB 411-837} Length = 837	gi|3220164	553	1530	97	97	HCGLC82
666	841181			2	283			HCFMN22
667	841182	70 K protein (AA 1-614) [Homo sapiens] >pir|A25707|A25707 U1 snRNP 70K protein - human >gi|337447 small ribonucleoprotein 70 kd protein [Homo sapiens] {SUB 178-614} >gi|602021 hU1-70K protein (302 AA) [Homo sapiens] {SUB 227-527} Length = 614	gi|36100	251	988	100	100	HCFNJ56
668	841185			342	536			HCFNF67
669	841187			458	1096			HCGAA74
670	841188	DNA repair endonuclease subunit [Homo sapiens] Length = 905	gi|1524411	2	2749	92	92	HCFMK76
671	841189			336	926			HCFMC34

672	841192	methylmalonyl-CoA mutase [Homo sapiens] >sp|P22033|MUTA_HUMAN METHYLMALONYL-COA MUTASE PRECURSOR (EC 5.4.99.2) (MCM). Length = 750	gi|187452	1	1428	99	99	HCFMO54
673	841194	(AF039405) arsenite-translocating ATPase [Mus musculus] >sp|O54984|O54984 ARSENITE-TRANSLOCATING ATPASE. Length = 350	gi|2745900	182	1138	95	95	HCGAB52
674	841195			3	623			HCEWM29
675	841198			2	913			HCFBC32
676	841200	(AF015037) endooligopeptidase A related protein; EOPA related protein [Oryctolagus cuniculus] >sp|O46480|O46480 ENDOOLIGOPEPTIDASE A RELATED PROTEIN (FRAGMENT). Length = 667	gi|2827886	35	703	75	81	HCEER84
677	841201			158	571			HCEBD63
678	841202	rhoB [Homo sapiens] >gi|206656 rhoB [Rattus norvegicus] >gnl|PID|e258480 RHOB [Mus musculus] >pir|A01372|TVHURH GTP-binding protein rhoB - human >pir|A39727|TVRTRH GTP-binding protein rhoB - rat >pir|JC5075|JC5075 GTP-binding protein rhoB - mouse >gi|3373	gi|36032	66	1229	100	100	HCHOV21
679	841209			1	552			HCDME27
680	841210	PTB-associated splicing factor [Homo sapiens] >pir|A46302|A46302 PTB-associated splicing factor, long form - human >gi|23712 myoblast antigen 24.1D5 [Homo sapiens] {SUB 312-707} >gi|4063717 (AF110499) PTB-associated splicing factor [Mus musculus] {SUB 377	gi|38458	2	1405	93	93	HCEMT64

681	841213	G9a [Homo sapiens] >pir|S30385|S30385 G9a protein - human >sp|Q14349|Q14349 G9A PROTEIN CONTAINING ANKYRIN-LIKE REPEATS. Length = 1001	gi|287865	3	344	82	84	HCEFE38
682	841217			2	1198			HCE1V79
683	841219	SMOOTH MUSCLE MYOSIN HEAVY CHAIN (FRAGMENT). Length = 1052	sp|D1037960|D1037960	208	774	95	97	HBZSI02
684	841222			29	856			HCDCI63
685	841223			2088	2486			HCEBW38
686	841224	RNA polymerase II elongation factor ELL2 [Homo sapiens] >sp|O00472|ELL2_HUMAN RNA POLYMERASE II ELONGATION FACTOR ELL2. Length = 640	gi|1946347	2	2032	95	95	HCE2D15
687	841226			2	373			HCCMD50
688	841227			1	831			HBZAK55
689	841228	F25H9.7 [Caenorhabditis elegans] >gnl|PID|e1346003 F25H9.7 [Caenorhabditis elegans] >sp|P91989|P91989 F25H9.7 PROTEIN. Length = 154	gnl|PID|e1346003	3	407	46	62	HCDEA07
690	841231			279	977			HB3XCC66

691	841232	MHC HLA-RD protein [Homo sapiens] >pir|A33640|A33640 class III histocompatibility antigen RD - human Length = 382	gi|386949	3	461	94	95	HCE1S91
692	841233	(AF069984) nitrilase homolog 1 [Homo sapiens] >gi|3228666 (AF069987) nitrilase 1 [Homo sapiens] >sp|O76091|O76091 NITRILASE HOMOLOG 1. Length = 327	gi|3242978	2	673	94	95	HBUAF56
693	841234	(AJ005073) Alix [Mus musculus] >sp|O88695|O88695 ALIX. Length = 869	gnl|PID|e1318710	561	2564	89	91	HBWC170
694	841236			187	483			HBXGB85
695	841238			168	389			HBXFF92
696	841239			405	605			HBMUU08
697	841242			169	360			HBNAT03
698	841243			3	281			HBMTQ45
699	841248	phorbolin 3 [Homo sapiens] >sp|G4097433|G4097433 PHORBOLIN 3. Length = 235	gi|4097433	3	668	46	62	HBUAC02
700	841250			2	1309			HBJEC31
701	841251			5	247			HBJLL24
702	841254			879	1136			HBZSH07
703	841263			1	354			HBJDS57
704	841266			182	337			HBJFN11
705	841269	(AL021958) fadE9 [Mycobacterium tuberculosis] >sp|O53815|O53815 ACYL-COA DEHYDROGENASE. Length = 390	gnl|PID|e1253290	93	1130	51	70	HBDAC79
706	841272	p67 myc protein [Homo sapiens] >sp|D1001846|D1001846 P67 MYC PROTEIN (FRAGMENT). Length = 454	gnl|PID|d1001846	20	622	100	100	HBJFJ36
707	841273			697	948			HBFMD57
708	841276			244	423			HBNAE62

709	841277	NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-39KD) (CI-39KD). >gi|189049 NADH dehydrogenase (ubiquinone) [Homo sapiens] (SUB 3-377} Length = 377	sp|Q16795|NUEM_HUMAN	2	1171	94	94	HBICG75
710	841278	gag polyprotein - human endogenous virus S71 Length = 608	pir|A46312|A46312	119	415	44	56	HA1DB46
711	841279			187	645			HPIAF81
712	841280	(AF061513) candidate adaptor protein CED-6 [Caenorhabditis elegans] >sp|O76337|O76337 CANDIDATE ADAPTOR PROTEIN CED-6. Length = 492	gi|3253308	888	1823	50	69	HBCAS37
713	841282			219	368			HATAM48
714	841283			2530	2880			HBAFS89
715	841286	(AC003096) putative protein phosphatase 2C [Arabidopsis thaliana] >sp|O64583|O64583 HYPOTHETICAL 26.4 KD PROTEIN. Length = 239	gi|3132471	201	1319	57	80	HAHCP59
716	841287			3	248			HARMV18
717	841288	(AL021428) hypothetical protein Rv0068 [Mycobacterium tuberculosis] >sp|O53613|O53613 OXIDOREDUCTASE. Length = 303	gnl|PID|e1245998	3	821			HARMM85
718	841291	selenoprotein P [Homo sapiens] Length = 381	gnl|PID|e1192260	293	1012	88	89	HBMCL13
719	841292	SSR gamma subunit [Rattus norvegicus] >pir|S33294|S33294 translocon-associated protein gamma chain - rat Length = 185	gi|312702	2	664	98	98	HARAI52
720	841294	microtubule associated protein [Homo sapiens] >pir|I37356|I37356 epithelial microtubule-associated protein, 115K - human >sp|Q14244|Q14244 MICROTUBULE ASSOCIATED PROTEIN. Length = 749	gi|414115	3	1265	99	99	HAPOR25

721	841296	protein disulfide isomerase-related protein [Homo sapiens] >pir|A23723|A23723 protein disulfide-isomerase (EC 5.3.4.1) ERp72 precursor - human >sp|P13667|ER72_HUMAN PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72). Length = 645	gi|181508	2	1405	96	96	HASAS34
722	841298	Gps1 [Homo sapiens] >pir|G01646|G01646 Gps1 - human >sp|Q13098|GPS1_HUMAN G PROTEIN PATHWAY SUPPRESSOR 1 (GPS1 PROTEIN) (MFH PROTEIN). {SUB 30-500} Length = 500	gi|644879	3	1067	91	91	HATAI49
723	841301			10	231			HAPNO69
724	841303	synexin [Homo sapiens] >sp|P20073|ANX7_HUMAN ANNEXIN VII (SYNEXIN). Length = 466	gi|338244	3	1457	100	100	HAOMG39
725	841304	(AB000199) CCA2 protein [Rattus norvegicus] >sp|O35048|O35048 CCA2 PROTEIN. Length = 338	dbj|AB000199_1	3	707	89	95	HAPOE40
726	841305			399	1274			HAMHD70
727	841309	similar to RNA binding protein; >sp|Q19706|IF35_CAEEL PROBABLE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 RNA-BINDING SUBUNIT (EIF-3 RNA-BINDING SUBUNIT) (EIF3 P33) (TRANSLATION INITIATION F	gnl|PID|e1345859	137	1699	48	63	HAPAJ60
728	841314			3	920			HAMGN09
729	841316	(AJ224819) tumor suppressor [Homo sapiens] >sp|O60858|O60858 TUMOR SUPPRESSOR. Length = 407	gnl|PID|e1292742	185	1420	93	93	HAJCP55

730	841318	replication control protein 1 [Homo sapiens] >pir|G02329|G02329 replication control protein 1 - human >sp|Q13471|Q13471 REPLICATION CONTROL PROTEIN 1. Length = 861	gi|1171204	170	436	100	100	HAMFQ80
731	841321	hnRNP A2 protein [Homo sapiens] >gnl|PID|d1006583 hnRNP A2 protein [Homo sapiens] >gi|500638 hnRNP protein A2 [Homo sapiens] Length = 341	gi|337449	3	656	100	100	HBJMK69
732	841324	chimeric IFNalpha/beta-receptor [Homo sapiens] >gi|306914 interferon-alpha receptor precursor [Homo sapiens] >pir|A32694|A32694 interferon alpha receptor precursor - human >sp|P17181|INR1_HUMAN INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALP	gnl|PID|e251628	31	1755	99	99	HAMGF04
733	841326	Rch1 [Homo sapiens] >gi|899539 hSRP1alpha [Homo sapiens] >pir|A56516|A56516 nuclear localization sequence receptor SRP1 alpha - human >sp|P52292|IMA2_HUMAN IMPORTIN ALPHA-2 SUBUNIT (KARYOPHERIN ALPHA-2 SUBUNIT) (SRP1-ALPHA) (RAG COHORT PROTEIN 1). Length	gi|791185	3	1715	97	97	HAMFV20
734	841328	nuclear ribonucleoprotein [Homo sapiens] >gi|35772 polypirimidine tract binding protein [Homo sapiens] >pir|S26294|S26294 polypyrimidine tract-binding protein - human Length = 557	gi|32354	2	1126	89	89	HAMGF52
735	841329	dJ434P1.3 [Homo sapiens] >gi|1592565 DEAD-box protein p72 [Homo sapiens] >pir|S72367|S72367 ATP-dependent RNA helicase - human >sp|Q92841|P72_HUMAN PROBABLE RNA-DEPENDENT HELICASE	gnl|PID|e1249592	93	671	100	100	HAJBV54

P72 (DEAD-BOX PROTEIN P72). Length = 650

736	841330	(AF002228) tbx3 [Homo sapiens] >sp|O15119|O15119 TBX3 (FRAGMENT). Length = 468	gi|3041821	3	1097	91	91	HAJAZ71
737	841333	(AB010882) hSNF2H [Homo sapiens] >sp|O60264|O60264 HSNF2H. Length = 1052	gnl|PID|d1026101	1	2004	92	92	HAJBA64
738	841334	SDF2 [Mus musculus] >pir|JC5105|JC5105 stromal cell-derived factor 2 - mouse >sp|P97307|P97307 STROMAL CELL DERIVED FACTOR 2 (SDF2). Length = 211	gnl|PID|d1009954	3	713	59	71	HAJBE68
739	841335			443	946			HAJAT72
740	841336			1	1557			HAJCD33
741	841337			263	1375			HAJAO95
742	841339	transcription factor SC1 [Homo sapiens] >sp|Q13176|Q13176 TRANSCRIPTION FACTOR SC1. Length = 359	gi|833833	27	740	88	89	HAJCB95
743	841340			820	1017			HAJAD20
744	841341			3	359			HAJAL18
745	841342			1145	1417			HAJAI64
746	841343	cellular nucleic acid binding protein [Mus musculus] >pir|I49259|I49259 cellular nucleic acid binding protein - mouse Length = 178	gi|854675	263	685	100	100	HAMGG35
747	841347	(AF038844) MKP-1 like protein tyrosine phosphatase [Homo sapiens] >sp|G4104681|G4104681 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE. Length = 198	gi|4104681	161	409	100	100	HAHSE21

748	841352	ribosomal protein L35 [Homo sapiens] >pir|G01477|G01477 ribosomal protein L35 - human Length = 123	gi|562074	3	461	100	100	HBJJF14
749	841353			73	462			HAICO69
750	841354			115	630			HAPNQ64
751	841360			1	816			HAMFM60
752	841366	FKBP65 binding protein [Mus musculus] >pir|I49669|I49669 FKBP65 binding protein - mouse >sp|Q61576|Q61576 FK506 BINDING PROTEIN 6 (65 KDA) (FKBP65 BINDING PROTEIN). Length = 581	gi|894162	222	1319	92	96	HAMGA45
753	841405	cathepsin O [Homo sapiens] >gi|562757 Cathepsin O [Homo sapiens] >bbs|172248 cathepsin O2 [human, spleen, Peptide, 329 aa] [Homo sapiens] >pir|JC2476|JC2476 cathepsin K (EC 3.4.22.-) precursor - human	gi|606923	24	1106	100	100	HOABW85
754	841526	signal recognition particle receptor beta subunit [Mus musculus] >pir|A56487|A56487 signal recognition particle receptor beta chain - mouse Length = 269	gi|600886	3	848	86	88	HABAD39
755	841712			3	698			HBJJT93
756	841860			1984	2352			HPIAP58
757	842042	DNA-binding protein [Homo sapiens] >pir|S69501|S69501 DNA-binding protein A variant - human >sp|Q14121|Q14121 DNA-BINDING PROTEIN. Length = 372	gnl|PID|e219699	2	817	76	76	HBMXV50
758	842453	mitochondrial ATPase inhibitor [Rattus norvegicus] >gnl|PID|d1002924 ATPase inhibitor protein precursor [Rattus sp.] >pir|JS0738|JS0738 ATPase inhibitor protein precursor, mitochondrial - rat >sp|Q03344|IATP_RAT ATPASE INHIBITOR, MITOCHONDRIAL	gi|517226	13	276	76	88	HBKDV52

PRECURSOR.

759	842635			268	936			HFHH20
760	842927			2	1630			HCE3G66
761	842988			940	1152			HOSAB76
762	843080			2050	2442			HDPBA08
763	843237			370	1359			HETIJ27
764	843381			520	777			HSIGN74
765	843718	(AF010313) Pig8 [Homo sapiens] >sp|O14681|O14681 PIG8. Length = 318	gi|2415302	212	262	100	100	HMEG184
766	843823			2	1414			HHESE85
767	844056	(AF010187) FGF-1 intracellular binding protein [Homo sapiens] >gi|2738522 (AF010188) FGF-1 intracellular binding protein [Cercopithecus aethiops] >gi|2738520 (AF010187) FGF-1 intracellular binding protein [Homo sapiens] >gi|2738522 (AF010188) FGF-1 intrac	gi|2738520	2	751	100	100	HE8UZ38
768	844325	(AF059569) actin binding protein MAYVEN [Homo sapiens] >sp|G3789797|G3789797 ACTIN BINDING PROTEIN MAYVEN. Length = 593	gi|3789797	46	1056	37	61	HPRSB90
769	844344	heparin-binding fibroblast growth factor receptor 2 [Rattus norvegicus] >sp|Q63241|Q63241 HEPARIN-BINDING FIBROBLAST GROWTH FACTOR RECEPTOR 2 (FRAGMENT). {SUB 1-330} Length = 331	gi|310149	1	303	40	60	HBJNC37
770	844368	15 KDA SELENOPROTEIN. Length = 162	sp|O60613|O60613	3	374	91	91	HAGHY70

771	844408	(AF001437) dihydrolipoamide dehydrogenase-binding protein [Homo sapiens] Length = 501	gi|2316040	1358	1651	100	100	HTNAD87
772	844508			1	300			HADGG65
773	844867			174	371			HMVBJ82
774	845000			1	321			HE9DB89
775	845281	pre-pro polypeptide (AA -25 to 451) [Homo sapiens] >pir|S09489|S09489 carboxypeptidase H (EC 3.4.17.10) precursor - human >sp|P16870|CBPH_HUMAN CARBOXYPEPTIDASE H PRECURSOR (EC 3.4.17.10) (CPH) (CARBOXYPEPTIDASE E) (CPE) (ENKEPHALIN CONVERTASE) (PROHORMON	gi|29667	3	1475	100	100	HEGAE94
776	845288	(AF023268) propin1 [Homo sapiens] Length = 347	gi|2564915	571	1107	75	76	HTLDM37
777	845750	selenium-binding protein [Homo sapiens] >pir|G01872|G01872 selenium-binding protein - human >sp|Q13228|Q13228 SELENIUM-BINDING PROTEIN. Length = 472	gi|1374792	3	1499	95	96	HE9DH28
778	845809	SNAP23A protein [Homo sapiens] >gnl|PID|e1331767 (AJ011915) synaptosome associated protein of 23 kilodaltons, isoform A [Homo sapiens] >pir|JC5296|JC5296 vesicle-membrane fusion protein SNAP-23A - human >sp|O00161|O00161 VESICLE-MEMBRANE FUSION PROTEIN SN	gnl|PID|e290695	134	772	100	100	HRGSE41
779	846077			182	487			HCNCN11
780	HPFCH77R			21	80			HPFCH77
781	HPRTI05R			2	151			HPRTI05
782	HMSKI93R			25	192			HMSKI93

783	HKAAC88R	(AB003103) 26S proteasome subunit p55 [Homo sapiens] >sp|O00232|O00232 PROTEASOME SUBUNIT P55. Length = 456	gnl|PID|d1020530	1	333	85	88	HKAAC88
784	HPDED94R	(AF001212) 26S proteasome subunit 9 [Homo sapiens] >sp|O00495|O00495 26S PROTEASOME SUBUNIT 9. Length = 422	gi|2150046	1	225	98	98	HPDED94
785	HDTGH11R	(AF009674) axin [Homo sapiens] >sp|O15169|O15169 AXIN (FRAGMENT). Length = 900	gi|2252820	1	189	96	96	HDTGH11
786	HTEJR60R	(AF022184) EZF [Homo sapiens] >sp|O43474|EZF_HUMAN EPITHELIAL ZINC-FINGER PROTEIN EZF. Length = 470	gi|2897954	2	511	77	77	HTEJR60
787	HAGGY86R	(AF029786) GBAS [Homo sapiens] >sp|O75323|O75323 GBAS. Length = 286	gi|3403167	2	295	97	98	HAGGY86
788	HPIAU47R	(AF031647) JAB1-containing signalosome subunit 3 [Homo sapiens] >sp|O43191|O43191 SIGNALOSOME SUBUNIT 3. Length = 403	gi|2688989	3	377	89	91	HPIAU47
789	HCGAD89R	(AF074935) beta-tubulin [Cryptosporidium parvum] >gi|3328337 (AF074936) beta-tubulin [Cryptosporidium parvum] >sp|O77467|O77467 BETA-TUBULIN (FRAGMENT). Length = 57	gi|3328335	226	390	86	89	HCGAD89
790	HAPOD39R	(AF089866) keratin 19 [Rattus norvegicus] >sp|G3766220|G3766220 KERATIN 19 (FRAGMENT). Length = 123	gi|3766220	3	386	88	93	HAPOD39
791	HOGAA68R	5' half of the product is homologues to Bacillus subtiis SAICAR synthetase, 3' half corresponds to the catalytic subunit of AIR carboxylase [Homo sapiens] >pir|S14147|S14147 multifunctional purine biosynthesis protein - human Length = 425	gi|28384	1	468	95	97	HOGAA68

792	HCLBO46R	Actin [Drosophila melanogaster] >pir|S14851|S14851 actin - fruit fly (Drosophila melanogaster) >sp|Q24228|Q24228 ACTIN. Length = 100	gi|7550	1	303	94	95	HCLBO46
793	HDRAA14R	ADP,ATP carrier protein T2 - human >sp|P12236|ADT3_HUMAN ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3). Length = 298	pir|S03894|S03894	2	304	80	92	HDRAA14
794	HSLCA48R	alpha-1 (III) collagen [Homo sapiens] Length = 1078	gi|930045	2	457	70	75	HSLCA48
795	HMEAC81R	alpha-subunit of G-protein, type G-alpha-i-1 [Xenopus laevis] >pir|S11045|RGXL11 GTP-binding regulatory protein Gi alpha-1 chain (adenylate cyclase-inhibiting) - African clawed frog >sp|P27044|GBI1_XENLA GUANINE NUCLEOTIDE-BINDING PROTEIN G(I), ALPHA-1 SU	gi|64708	99	176	92	92	HMEAC81
796	HMQDF20R	beta-1,2-N-acetylglucosaminyltransferase II [Homo sapiens] >pir|S66256|S66256 alpha-1,6-mannosyl-glycoprotein beta-1, 2-N-acetylglucosaminyltransferase (EC 2.4.1.143) - human >sp|Q10469|GNT2_HUMAN ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N- ACETYLGLUCOSAM	gi|902745	3	287	85	85	HMQDF20
797	HCHOH06R			12	242			HCHOH06
798	HDQMC20R			3	167			HDQMC20
799	HMKCW11R			2	112			HMKCW11

800	HLDRN91R	C4b-binding protein alpha chain [Homo sapiens] >gi|190502 C4b-binding protein alpha chain [Homo sapiens] >pir|A33568|NBHUC4 C4b-binding protein alpha chain precursor - human >sp|P04003|C4BP_HUMAN C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PRO	gi|190500	2	331	99	100	HLDRN91
801	HCHBR17R	cathepsin D [Homo sapiens] >gi|29678 precursor polypeptide (AA -20 to 392) [Homo sapiens] >gi|181180 preprocathepsin D [Homo sapiens] >pir|A25771|KHHUD cathepsin D (EC 3.4.23.5) precursor - human >sp|P07339|CATD_HUMAN CATHEPSIN D PRECURSOR (EC 3.4.23.5).	gi|179948	3	149	92	92	HCHBR17
802	HMKCH15R	Cbf5p homolog [Homo sapiens] Length = 514	gi|2737894	131	400	81	81	HMKCH15
803	HE6GO78R	clathrin light-chain A [Homo sapiens] Length = 218	gi|307118	155	502	80	83	HE6GO78
804	HSLF156R	complement component C3 [Homo sapiens] >pir|A94065|C3HU complement C3 precursor - human >sp|P01024|CO3_HUMAN COMPLEMENT C3 PRECURSOR [CONTAINS: C3A ANAPHYLATOXIN]. >gi|181130 complement component C3 [Homo sapiens] {SUB 1-24} Length = 1663	gi|179665	48	422	80	82	HSLF156
805	HSYBY17R	cyclin G [Homo sapiens] >gi|1236233 cyclin G1 [Homo sapiens] >gi|1236913 cyclin G1 [Homo sapiens] >pir|G02401|G02401 cyclin G1 - human >sp|P51959|CG2G_HUMAN G2/MITOTIC-SPECIFIC CYCLIN G1. >gnl|PID|d1013694 cyclin G [Homo sapiens] {SUB 1-279} >gi|1486361 c	gnl|PID|d1012016	79	300	100	100	HSYBY17

806	HPJCS07R	cytochrome oxidase I [Apteryx australis] >sp|O03515|COX1_APTAU CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT). Length = 337	gi|2198683	113	226	83	92	HPJCS07
807	HFADV82R	cytochrome oxidase III [Homo sapiens] >pir|A00482|OTHU3 cytochrome-c oxidase (EC 1.9.3.1) chain III - human mitochondrion (SGC1) >sp|P00414|COX3_HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE III (EC 1.9.3.1). >gi|2245564 (AF004341) cytochrome c oxidase subunit I	gi|13010	1	105	81	83	HFADV82
808	HFKFH08R	DNA polymerase delta small subunit [Homo sapiens] >pir|I38950|I38950 DNA-directed DNA polymerase (EC 2.7.7.7) delta regulatory chain - human >sp|P49005|DPD_HUMAN DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7). Length = 469	gi|1008458	2	550	97	98	HFKFH08
809	HMCDK47R	electron transport flavoprotein [Homo sapiens] >pir|A31998|A31998 electron transfer flavoprotein alpha chain precursor - human >sp|P13804|ETFA_HUMAN ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT PRECURSOR (ALPHA-ETF). >gnl|PID|e1331769 (AJ224002) electron	gi|182251	3	320	100	100	HMCDK47
810	HPIBI27R	elongation factor 2 [Homo sapiens] >gi|31108 human elongation factor 2 [Homo sapiens] >pir|S18294|EFHU2 translation elongation factor eEF-2 - human >sp|P13639|EF2_HUMAN ELONGATION FACTOR 2 (EF-2). >gi|181969 elongation factor 2 [Homo sapiens] {SUB 501-858	gi|31106	23	319	98	98	HPIBI27

811	HSKJG37R	elongation factor 2 [Homo sapiens] >gi|31108 human elongation factor 2 [Homo sapiens] >pir|S18294|EFHU2 translation elongation factor eEF-2 - human >sp|P13639|EF2_HUMAN ELONGATION FACTOR 2 (EF-2). >gi|181969 elongation factor 2 [Homo sapiens] {SUB 501-858	gi|31106	1	372	100	100	HSKJG37
812	H2LAZ24R	elongation factor-1-beta [Homo sapiens] >gi|31135 elongation factor 1-beta [Homo sapiens] >pir|S25432|S25432 translation elongation factor eEF-1 beta chain - human >sp|P24534|EF1B_HUMAN ELONGATION FACTOR 1-BETA (EF-1-BETA). {SUB 2-225} Length = 225	gi|31100	23	562	100	100	H2LAZ24
813	H2LAC50R	enhancer protein [Homo sapiens] >pir|I54533|I54533 enhancer protein - human Length = 199	gi|440306	38	415	100	100	H2LAC50
814	HPEAE15R	GLANDULAR KALLIKREIN-1. Length = 223	sp|Q15946|Q15946	51	236	80	80	HPEAE15
815	HPIAA24R	GTP-binding protein Ran/TC4 - mouse (fragment) Length = 70	pir|JH0654|JH0654	382	507	91	91	HPIAA24
816	H2LAS1R	guanylate cyclase (EC 4.6.1.2) - bovine (fragment) >gi|407777 guanylate cyclase [Bos taurus] {SUB 2-498} Length = 498	pir|S48119|S48119	28	549	100	100	H2LAS1
817	HHERW66R	HMG1 protein (AA 1 - 215) [Bos taurus] >pir|S01947|S01947 nonhistone chromosomal protein HMG-1 - bovine >sp|P10103|HMG1_BOVIN HIGH MOBILITY GROUP PROTEIN HMG1 (HMG-1). {SUB 2-215} Length = 215	gi|417	3	386	83	83	HHERW66

818	HADMC73R	hMn-superoxiddismutase [unidentified] >gi|491292 hMN-superoxiddismutase [unidentified] >gnl|PID|e93456 Mn-superoxiddismutase [Homo sapiens] {SUB 23-199} Length = 199	gi|491290	2	94	96	100	HADMC73
819	H6EEU22R	hormone receptor hERR1 (AA 1-521) [Homo sapiens] >pir|A29345|A29345 steroid hormone receptor ERR1 precursor - human >sp|P11474|ERR1_HUMAN STEROID HORMONE RECEPTOR ERR1 (ESTROGEN-RELATED RECEPTOR, ALPHA) (ESTROGEN RECEPTOR-LIKE 1). Length = 521	gi|36609	34	225	100	100	H6EEU22
820	HDTDX66R	HP1Hs-gamma [Homo sapiens] >sp|Q13185|HP1G_HUMAN HETEROCHROMATIN PROTEIN 1 HOMOLOG GAMMA (HP1 GAMMA) (MODIFIER 2 PROTEIN). >sp|G1773227|G1773227 HP1HS-GAMMA. Length = 173	gi|1773227	132	449	82	84	HDTDX66
821	HLPBB39R	human metallothionein-1e [Homo sapiens] >pir|A22634|SMHU1E metallothionein 1E - human >sp|P04732|MT1E_HUMAN METALLOTHIONEIN-1E (MT-1E). >bbs|144157 metallothionein MT-1e isoform, metallothionein-1e [human, monocytes, Peptide Partial, 31 aa] [Homo sapiens]	gi|386865	40	246	100	100	HLPBB39
822	HOELG04R	hypothetical 18K protein (rRNA) - goldfish mitochondrion (SGC1) Length = 166	pir|JC1348|JC1348	293	415	65	68	HOELG04

823	HKABU38R	initation factor 4B [Homo sapiens] >pir|S12566|S12566 translation initiation factor eIF-4B - human >sp|P23588|IF4B_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 4B (EIF-4B). Length = 611	gi|288100	2	463	92	92	HKABU38
824	HBGOI32R	keratin 18 [Homo sapiens] >gi|307081 keratin 18 precursor [Homo sapiens] >gi|34037 cytokeratin 18 [Homo sapiens] >pir|S05481|S05481 keratin 18, type I, cytoskeletal - human >sp|P05783|K1CR_HUMAN KERATIN, TYPE I CYTOSKELETAL 18 (CYTOKERATIN 18) (K18) (CK 1	gi|386844	1	240	66	67	HBGOI32
825	HATAI03R	KIAA0106 [Homo sapiens] >sp|P30041|AOP2_HUMAN ANTIOXIDANT PROTEIN 2 (EC 1.11.1.7) (24 KD PROTEIN) (LIVER 2D PAGE SPOT 40) (RED BLOOD CELLS PAGE SPOT 12). {SUB 2-224} Length = 224	gnl|PID|d1004007	3	194	90	93	HATAI03
826	HCEDE25R	KIAA0106 [Homo sapiens] >sp|P30041|AOP2_HUMAN ANTIOXIDANT PROTEIN 2 (EC 1.11.1.7) (24 KD PROTEIN) (LIVER 2D PAGE SPOT 40) (RED BLOOD CELLS PAGE SPOT 12). {SUB 2-224} Length = 224	gnl|PID|d1004007	2	283	100	100	HCEDE25
827	HKDBF62R	metallothionein-1G [Homo sapiens] >pir|A29236|SMHU1G metallothionein 1G - human >sp|P13640|MT1G_HUMAN METALLOTHIONEIN-1G (MT-1G). >bbs|144160 metallothionein MT-1g isoform, metallothionein-1g [human, monocytes, Peptide Partial, 31 aa] [Homo sapiens] {SUB	gi|188713	170	322	95	95	HKDBF62

828	HNTSX94R	mitochondrial matrix protein [Homo sapiens] >pir|A32800|A32800 chaperonin GroEL precursor - human >sp|P10809|P60_HUMAN MITOCHONDRIAL MATRIX PROTEIN PI PRECURSOR (P60 LYMPHOCYTE PROTEIN) (60 KD CHAPERONIN) (HEAT SHOCK PROTEIN 60) (HSP-60) (PROTEIN CPN60) (	gi|190127	3	431	97	100	HNTSX94
829	HRGBR08R	mitochondrial matrix protein [Homo sapiens] >pir|A32800|A32800 chaperonin GroEL precursor - human >sp|P10809|P60_HUMAN MITOCHONDRIAL MATRIX PROTEIN PI PRECURSOR (P60 LYMPHOCYTE PROTEIN) (60 KD CHAPERONIN) (HEAT SHOCK PROTEIN 60) (HSP-60) (PROTEIN CPN60) (	gi|190127	1	504	94	94	HRGBR08
830	H2LAO77R	MSS1 protein [Homo sapiens] >pir|S24353|S24353 proteasome 26S subunit MSS1 - human >sp|G385267|G385267 26 S PROTEASE SUBUNIT 7, MSS1=MODULATOR OF HIV TAT-MEDIATED TRANSACTIVATION. {SUB 2-23} Length = 433	gnl|PID|d1002345	137	580	91	91	H2LAO77
831	HNTRW15R	NAD+ ADP-ribosyltransferase [Homo sapiens] >pir|A29725|A29725 NAD+ ADP-ribosyltransferase (EC 2.4.2.30), nuclear - human >sp|P09874|PPOL_HUMAN POLY [ADP-RIBOSE] POLYMERASE (EC 2.4.2.30) (PARP) (ADPRT) (NAD(+) ADP-RIBOSYLTRANSFERASE) (POLY[ADP-RIBOSE] SYN	gi|178190	163	297	90	96	HNTRW15

832	HORBH08R	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 51K chain precursor - human (fragment) >sp|P49821|NUBM_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE 51 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-51KD) (CI-51KD) (FRAGMENT). >bbs|142159 NADH ubiquinone	pir|A44362|A44362	186	428	83	87	HORBH08
833	HULBL38R	nonstructural protein P125-2 [pestivirus type 1] >sp|O57114|O57114 NONSTRUCTURAL PROTEIN P125-2 (FRAGMENT). Length = 239	gi|2707597	3	437	95	97	HULBL38
834	HNTBK49R	p60 [Homo sapiens] >sp|Q13446|Q13446 EB[3-ASSOCIATED PROTEIN P60. >gi|3283216 (AF060494) ubiquitin binding protein p62 [Homo sapiens] {SUB 1-72} Length = 440	gi|1145799	3	368	100	100	HNTBK49
835	HBAFS48R	Phalaenopsis sp. 'hybrid SM9108' actin [Phalaenopsis sp. 'hybrid SM9108'] >sp|Q40981|Q40981 ACTIN (FRAGMENT). Length = 208	gi|602958	2	316	91	92	HBAFS48
836	HHGAL60R	PIPPin protein [Rattus norvegicus] >pir|JC4588|JC4588 RNA-binding protein PIPPin - rat >sp|Q63430|Q63430 PIPPIN PROTEIN. Length = 154	gi|1050754	2	319	66	81	HHGAL60
837	HOHBU75R	prepro-alpha-1 collagen [Homo sapiens] >sp|Q15201|Q15201 PREPRO-ALPHA-1 COLLAGEN PRECURSOR (FRAGMENT). Length = 181	gi|35658	104	373	71	72	HOHBU75
838	HHEFZ79R	progesterone-induced protein [Oryctolagus cuniculus] >pir|A26998|A26998 progesterone-induced protein, endometrial - rabbit Length = 370	gi|165009	293	484	73	77	HHEFZ79

839	HSLBA61R	protcasome subunit C5 [Homo sapiens] >gnl|PID|e1334433 (AL031259) C5 (proteasome subunit HC5) [Homo sapiens] >pir|S15973|SNHUC5 multicatalytic endopeptidase complex (EC 3.4.99.46) chain C5 - human >sp|P20618|PRC5_HUMAN PROTEASOME COMPONENT C5 (EC 3.4.99.4	gnl|PID|d1001116	45	224	96	96	HSLBA61
840	HPEAE18R	put. ORF [Homo sapiens] >pir|I38022|I38022 hypothetical protein - human >sp|Q29976|Q29976 MAHLAVU HEPATOCELLULAR CARCINOMA HHC(M) DNA. Length = 196	gi|288145	55	234	57	67	HPEAE18
841	HNGFO65R	ren(exclusion;96) [Bacteriophage lambda] >pir|F43010|ZRBPL ren protein - phage lambda Length = 96	gi|215152	3	203	48	59	HNGFO65
842	HKAKR61R	ribosmal protein small subunit [Homo sapiens] Length = 264	gi|306553	3	458	91	91	HKAKR61
843	H2LAP11R	ribosomal phosphoprotein P1 (AA 1-114) [Rattus rattus] >pir|S08022|R5RT12 acidic ribosomal protein P1 - rat Length = 114	gi|57710	169	549	100	100	H2LAP11
844	H2CBD90R	ribosomal protein L10 [Homo sapiens] >sp|D1026771|D1026771 RIBOSOMAL PROTEIN L15 (FRAGMENT). {SUB 16-57} Length = 205	gi|414587	199	501	95	95	H2CBD90
845	H2LAD40R	ribosomal protein L15 gene product [Rattus norvegicus] >pir|JC2369|JC2369 ribosomal protein L15 - rat Length = 204	gi|515865	156	524	100	100	H2LAD40

846	HCYBK51R	ribosomal protein L37 [Homo sapiens] >bbs|172744 ribosomal protein L37 {C2-C2 zinc-finger-like} [human, HeLa cells, Peptide, 97 aa] [Homo sapiens] >gnl|PID|d1005426 ribosomal protein L37 [Homo sapiens] >gi|57121 ribosomal protein L37 [Rattus norvegicus] >	gi|292441	2	412	97	98	HCYBK51
847	H2MBC73R	ribosomal protein L37a [Homo sapiens] >gi|36134 ribosomal protein L37a [Homo sapiens] >gi|57123 ribosomal protein L37a (AA 1 - 92) [Rattus rattus] >gi|312414 ribosomal protein L37a [Mus musculus] >pir|S05014|R5RT37 ribosomal protein L37a - rat >pir|S42109	gi|292439	2	385	100	100	H2MBC73
848	H2MBU27R	ribosomal protein L37a [Homo sapiens] >gi|36134 ribosomal protein L37a [Homo sapiens] >gi|57123 ribosomal protein L37a (AA 1 - 92) [Rattus rattus] >gi|312414 ribosomal protein L37a [Mus musculus] >pir|S05014|R5RT37 ribosomal protein L37a - rat >pir|S42109	gi|292439	2	286	100	100	H2MBU27
849	HDSAH53R	ribosomal protein L37a [Homo sapiens] >gi|36134 ribosomal protein L37a [Homo sapiens] >gi|57123 ribosomal protein L37a (AA 1 - 92) [Rattus rattus] >gi|312414 ribosomal protein L37a [Mus musculus] >pir|S05014|R5RT37 ribosomal protein L37a - rat >pir|S42109	gi|292439	3	341	97	97	HDSAH53
850	HAIDF69R	ribosomal protein L7a [Fugu rubripes] Length = 266	gnl|PID|e1248480	179	250	93	100	HAIDF69

851	HDBAA15R	ribosomal protein L8 [Homo sapiens] >gi|57704 ribosomal protein L8 [Rattus rattus] >gi|1527178 ribosomal protein L8 [Mus musculus] >pir|JU0177|R5RTL8 ribosomal protein L8, cytosolic - rat >pir|JN0923|JN0923 ribosomal protein L8, cytosolic - human >gi|3851	gi|433899	220	429	85	88	HDBAA15
852	HDTHW54R	ribosomal protein S12 (AA 1 - 132) [Mus musculus] >pir|S13074|R3RT12 ribosomal protein S12 - rat >pir|S05492|R3MS12 ribosomal protein S12 - mouse >gi|206741 ribosomal protein S12 [Rattus norvegicus] {SUB 1-130} Length = 132	gi|54006	3	332	89	89	HDTHW54
853	HTWJC11R	ribosomal protein S13 [Homo sapiens] >gi|488417 ribosomal protein S13 [Homo sapiens] >gnl|PID|d1014222 ribosomal protein S13 [Homo sapiens] >gi|57730 ribosomal protein S13 [Rattus rattus] >pir|S34109|S34109 ribosomal protein S13, cytosolic - human >pir|A3	gi|307391	1	276	97	97	HTWJC11
854	HKAEC40R	ribosomal protein S24 [Homo sapiens] >gi|517222 ribosomal protein S24 [Homo sapiens] >gi|49652 ribosomal protein S19 (AA 1 - 133) [Mesocricetus auratus] >gi|57858 ribosomal protein S24 [Rattus norvegicus] >gi|57722 ribosomal protein S24 (AA 1-133) [Rattus	gi|337506	93	407	83	84	HKAEC40
855	HCFNM70R	ribosomal protein S4X isoform [Homo sapiens] >gi|2791861 (AF041428) ribosomal protein s4 X isoform [Homo sapiens] >gi|200864 ribosomal protein S4 [Mus musculus] >gi|57135 ribosomal protein S4 (AA 1 - 263) [Rattus rattus] >gnl|PID|d1002335 ribosomal protei	gi|337510	3	278	96	97	HCFNM70

856	HKBAB93R	ribosomal protein S8 [Homo sapiens] >gi|57139 ribosomal protein S8 (AA 1-208) [Rattus norvegicus] >gi|313298 ribosomal protein S8 [Mus musculus] >pir|S01609|R3RT8 ribosomal protein S8 - rat >pir|S42110|S42110 ribosomal protein S8 - mouse >pir|S25022|S2502	gi|36150	2	391	87	90	HKBAB93
857	HLHEJ79R	RNA polymerase II subunit hRPB17 [Homo sapiens] >pir|S55370|S55370 RNA polymerase II chain hRPB17 - human Length = 150	gi|854177	129	446	83	86	HLHEJ79
858	HBGOI24R	S19 ribosomal protein [Homo sapiens] >pir|I52692|I52692 ribosomal protein S19, cytosolic - human Length = 145	gi|337733	2	421	99	100	HBGOI24
859	HNDAD16R	secretory protein [Homo sapiens] >gi|940946 intestinal trefoil factor [Homo sapiens] >pir|A48284|A48284 intestinal trefoil factor 3 precursor - human >sp|Q07654|ITF_HUMAN INTESTINAL TREFOIL FACTOR PRECURSOR (HPI.B). Length = 80	gi|402483	3	380	71	78	HNDAD16
860	HMAEA94R	serine/threonine protein kinase [Homo sapiens] >gnl|PID|e1154172 (AJ000512) serine/threonine protein kinase [Homo sapiens] Length = 431	gnl|PID|e293330	3	422	95	95	HMAEA94
861	HMWEA08R	signal recognition particle subunit 9 [Homo sapiens] >pir|A57292|A57292 signal recognition particle protein SRP9 - human Length = 86	gi|897851	119	394	90	93	HMWEA08
862	H6BSO48R	similar to Drosophila photoreceptor cell-specific protein, calphotin. [Homo sapiens] >sp|Q14676|Q14676 KIAA0170 PROTEIN. Length = 2089	gnl|PID|d1012153	1	528	95	95	H6BSO48

863	HRACC09R	smooth muscle protein [Homo sapiens] >pir|JS0774|JS0774 smooth muscle protein SM22 - human Length = 201	gi|177175	1	117	100	100	HRACC09
864	HOEEC67R	smooth muscle protein SM22 homolog - mouse Length = 201	pir|A60598|A60598	105	230	100	100	HOEEC67
865	HPFEA40R	t-complex polypeptide 1 (AA 1-556) [Homo sapiens] Length = 556	gi|36796	3	497	98	99	HPFEA40
866	HODAV31R	tissue inhibitor of metalloproteinases [Homo sapiens] Length = 166	gnl|PID|d1002390	1	273	64	67	HODAV31
867	HHEC189R	transaldolase [Homo sapiens] >gi|2612879 (AF010400) transaldolase-related protein [Homo sapiens] >sp|O00751|O00751 TRANSALDOLASE (EC 2.2.1.2). >gi|1480787 transaldolase [Homo sapiens] {SUB 302-337} Length = 337	gi|2073541	3	371	99	99	HHEC189
868	HSDFV03R	translocase [Bos taurus] >pir|B43646|B43646 ADP,ATP carrier protein T2 - bovine >sp|P32007|ADT3_BOVIN ADP,ATP CARRIER PROTEIN, ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3). Length = 298	gi|529417	20	412	92	96	HSDFV03
869	HTXPN01R	triosc-phosphate isomerase [Pan troglodytes] >gi|37247 triosephosphate isomerase [Homo sapiens] >gi|1200507 triosephosphate isomerase [Homo sapiens] >gi|339841 triosephosphate isomerase (EC 5.3.1.1) [Homo sapiens] >pir|S29743|ISHUT triose-phosphate isomer	gi|176960	3	281	98	98	HTXPN01
870	HHPSA49R	tuberin [Homo sapiens] Length = 1784	gi|450352	2	451	69	69	HHPSA49
871	H12LAT88R	type II mesothelial keratin K7 [Homo sapiens] >sp|Q92676|Q92676 MESOTHELIAL KERATIN K7 (TYPE II) (FRAGMENT). Length = 489	gi|386851	1	567	91	91	H12LAT88

872	H6EAD58R	49	174	H6EAD58
873	HACBH95R	2	364	HACBH95
874	HACBY16R	1	84	HACBY16
875	HAGCI33R	2	238	HAGCI33
876	HAHAD34R	61	123	HAHAD34
877	HAJAN69R	67	294	HAJAN69
878	HALSG52R	41	268	HALSG52
879	HAPPR17R	180	311	HAPPR17
880	HAQCG78R	3	110	HAQCG78
881	HAUBY86R	23	118	HAUBY86
882	HAVAA34R	1	117	HAVAA34
883	HBAFK20R	2	355	HBAFK20
884	HBGBE20R	31	315	HBGBE20
885	HBJBR66R	2	52	HBJBR66
886	HBJMU59R	2	208	HBJMU59
887	HBKDK63R	147	647	HBKDK63
888	HBMVT43R	2	70	HBMVT43
889	HCDAM59R	21	125	HCDAM59
890	HCFLN25R	3	224	HCFLN25
891	HCQAW59R	1	129	HCQAW59
892	HDPMA46R	223	420	HDPMA46
893	HDTAQ26R	177	296	HDTAQ26
894	HDTAT40R	1	213	HDTAT40
895	HDTLD39R	323	496	HDTLD39
896	HE2PO63R	39	278	HE2PO63
897	HELCV09R	1	72	HELCV09
898	HELHK95R	3	383	HELHK95
899	HEMGL70R	2	172	HEMGL70
900	HETIU72R	2	100	HETIU72
901	HFFAS19R	2	256	HFFAS19
902	HFTY465R	68	259	HFTY465

903	HFXAF89R	143	361	HFXAF89
904	HHEPR03R	89	307	HHEPR03
905	HHGAQ80R	2	202	HHGAQ80
906	HHSEF82R	170	304	HHSEF82
907	HKBAA63R	239	469	HKBAA63
908	HKIXQ47R	2	94	HKIXQ47
909	HLDNF70R	3	176	HLDNF70
910	HLQFO33R	62	268	HLQFO33
911	HLWBC80R	46	543	HLWBC80
912	HLYAV50R	3	224	HLYAV50
913	HMEKY67R	3	302	HMEKY67
914	HMTBN58R	3	377	HMTBN58
915	HNGAZ91R	22	276	HNGAZ91
916	HNTAC06R	2	133	HNTAC06
917	HOGAF41R	1	228	HOGAF41
918	HOUDQ92R	75	323	HOUDQ92
919	HPEAD91R	60	233	HPEAD91
920	HPIAF72R	128	310	HPIAF72
921	HPIAU01R	122	334	HPIAU01
922	HPIAU73R	99	275	HPIAU73
923	HPIAW19R	102	350	HPIAW19
924	HPIAZ19R	238	348	HPIAZ19
925	HPIBA31R	245	367	HPIBA31
926	HPIBS06R	84	182	HPIBS06
927	HPICB65R	2	430	HPICB65
928	HPIBJ22R	220	330	HPIBJ22
929	HPIBZ81R	214	384	HPIBZ81
930	HRACF81R	1	189	HRACF81
931	HRACT28R	110	319	HRACT28
932	HSBAP03R	123	263	HSBAP03
933	HSDJK57R	234	458	HSDJK57

934	HSIFY54R			1	321			HSIFY54
935	HSLDJ92R			24	275			HSLDJ92
936	HSLJI47R			185	379			HSLJI47
937	HTSGE55R			36	209			HTSGE55
938	HUFAT72R			276	410			HUFAT72
939	HULAI70R			176	337			HULAI70
940	HTGFW12R	yeast mismatch repair gene PMS1 homologue [Homo sapiens] >gnl|PID|d1008050 homologue of yeast PMS1 [Homo sapiens] >sp|Q16530|Q16530 PMS3 MRNA (YEAST MISMATCH REPAIR GENE PMS1 HOMOLOGUE), PARTIAL CDS (C-TERMINAL REGION) (FRAGMENT). Length = 256	gnl|PID|d1008092	3	233	94	97	HTGFW12

The first column of Table 1 shows the "SEQ ID NO:" for each of the 940 prostate cancer antigen polynucleotide sequences of the invention.

The second column in Table 1, provides a unique "Sequence/Contig ID" identification for each prostate and/or prostate cancer associated sequence. The third column in Table 1, "Gene Name," provides a putative identification of the gene based on the sequence similarity of its translation product to an amino acid sequence found in a publicly accessible gene database, such as GenBank (NCBI). The great majority of the cDNA sequences reported in Table 1 are unrelated to any sequences previously described in the literature. The fourth column, in Table 1, "Overlap," provides the database accession no. for the database sequence having similarity. The fifth and sixth columns in Table 1 provide the location (nucleotide position nos. within the contig), "Start" and "End", in the polynucleotide sequence "SEQ ID NO:X" that delineate the preferred ORF shown in the sequence listing as SEQ ID NO:Y. In one embodiment, the invention provides a protein comprising, or alternatively consisting of, a polypeptide encoded by the portion of SEQ ID NO:X delineated by the nucleotide position nos. "Start" and "End". Also provided are polynucleotides encoding such proteins and the complementary strand thereto. The seventh and eighth columns provide the "% Identity" (percent identity) and "% Similarity" (percent similarity) observed between the aligned sequence segments of the translation product of SEQ ID NO:X and the database sequence.

The ninth column of Table 1 provides a unique "Clone ID" for a clone related to each contig sequence. This clone ID references the cDNA clone which contains at least the 5' most sequence of the assembled contig and at least a portion of SEQ ID NO:X was determined by directly sequencing the referenced clone. The reference clone may have more sequence than described in the sequence listing or the clone may have less. In the vast majority of cases, however, the clone is believed to encode a full-length polypeptide. In the case where a clone is not full-length, a full-length cDNA can be obtained by methods described elsewhere herein.

Table 3 indicates public ESTs, of which at least one, two, three, four, five, ten, or more of any one or more of these public ESTs are optionally excluded from the invention.

SEQ ID NO:X (where X may be any of the polynucleotide sequences disclosed in the sequence listing as SEQ ID NO:1 through SEQ ID NO:940) and the translated SEQ ID NO:Y (where Y may be any of the polypeptide sequences disclosed in the sequence listing as SEQ ID NO:941 through SEQ ID NO:1880) are sufficiently accurate and otherwise suitable for a